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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nu	nucleic search, using sw model
Run on:	March 31, 2004, 13:52:29 ; Search time 3483 Seconds (without alignments) 7167.840 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-975-856-1 576 1 ATGAACGGAGGCCTTATGACGAGTAACTCCCCTCG 576
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 seqs, 21671516995 residues
Total number of	hits satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: 0 length: 200000000
Post-processing	<pre>: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</pre>
Database :	GenEmbl:* 1. gb ba:* 2. gb ba:* 3. gb htg:* 5. gb ow:* 6. gb pat:* 6. gb pat:* 7. gb pat:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

G 	Description	Seque	AR182977 Sequence	AR305671 Sequence	AX740218 Sequence	BD218420 SSX gene,	U90841 Homo sapien	A48452 Sequence 17	AX821947 Sequence	X86175 H.sapiens m	AR025465 Sequence AR060380 Sequence	AR117874 Sequence	AR167453 Sequence	1833/6 Sequence 2	AR305668 Sequence	AX114023 Sequence	AX719099 Sequence RD218417 SSX gene.	AX331558 Sequence	AX331950 Sequence	249105 h.Bapiens h U90840 Homo sapien	BC016957 Homo sapi	BC007343 Homo sapi	S824/1 HOMO Saptem	AR170504 Sequence	AR182978 Sequence	AR305672 Sequence	BD096873 Isolated	BD218421 SSX gene,	BC001003 Homo sapi	M46430 Sequence 13	AR167452 Sequence		AX821946 Sequence RD218416 SSX gene.		Ното вар			linear PAT 17-DEC-2001					τς 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	·, Ota, b.o.	r in a sample by
SUMMARIES	1.D	AR167456	AR182977	AR305671	AX740218 BD096872	BD218420	HSU90841	BC005325 A48452	AX821947	HSSSX2	AR025465 AR060380	AR117874	AR167453	1833/8 2031/96	AR305668	AX114023	AX719099 BD218417	AX331558	AX331950	HSU90840	BC016957	BC007343	3824/1 28167457	AR170504	AR182978	AR305672	AA/40213 BD096873	BD218421	BC001003	A48450 HSTI90842	AR167452	AR305667	AX821946 BD218416	HSSSX1	BC016640	ALIGNMENTS		576 hn DNA	US 6287756.	237			1 1 1	, Salltill, U.,	ing presence of cancer on of an SSX gene
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Gure, A.O., Tureci, O., Sahin, U., Tsang, S.,
Pfreundschuh, M., Old, L.J. and Chen, Y.-T.
SSX family proteins
Patent: US 6329140-A 1 15-JAN-2002,
Location/Qualifiers
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/organism="unknown"
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(I (bases 1 to 576)

Gure,A.O., Turecti,O., Sahin,U., Tsang,S.,

Pfreundschuh,M., Old,L.J. and Chen,Y.-T.

Isolated nucleic acid molecules encoding.
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Sequence 1 from patent US 6291658.
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/trānslation="MNGDDAFARRPRDDAQISEKLRKAFDDIAKYFSKKEWEKMKSSE
KIVYYWKLMYNTKLGFKYTLPPPRNSKRAADFHGNDFGNDRNHRNQVERPQMTFG
SLORIFPKIMPKKPABEENGLKEVPBASGPQNDGKQLCPPGNPSTLEKINKTSGPKRG
KHAWTHRLRBRKQLVYYEBISDPBEDDE"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                      AAATCCICGGAGAAAATCGICTATGIGITATGAAGCTAAAACTATGAGGTCATGACTAAAA
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                                                                    CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGGCTGCAGACTTCCAC
                                                                                        CTAGGITTCAAGGICACCCTCCCACCTTTCATGCGTAAGGAAACGGGCTGCAGACTTCCAC
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/db_xref="GI:30519359"
/db_xref="REMIREMBL:CAD90570"
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/organism="Homo sapiens"
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Sequence 1 from Patent EP1300463.
AX740218 GI:30519358
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/db_xref="taxon:9606"
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/codon_start=1
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Location/Qualifiers
1. 576
/organism="unknown"
/mol_type="genomic DNA"
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Tureci,O., Sahin,U., Pfreundschuh,M., Rammensee,H.G.
Stevanovic,S.
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ilarity 100.0%;
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BD218420 SX gene, method of determining the occurrence of cancer in sample by determining the expression of peptides originating in the SSX BD218420 BD218420 GI:33028190 BD218420 GI:33028190 BD218420 GI:33028190 BD218420 GI:33028190 BD218420 GI:33028190 BD218420 GI:33028190 GI:3302
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          Topology: Linear;
Isolated nucleic acid molecules encoding SSX family members
and uses
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1. .576
/organism='Unidentified'
Location/Qualifiers
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llarity 100.0%; Pred. No. 2.6e-164;
Conservative 0; Mismatches 0;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
       Strandedness: Single;
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Matches 576;
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Gure, N.C., Tureci, O., Sahin, U., Tsang, S., Scanlan, M.J., Knuth, A.
Pfreundschuh, Old, L.J. and Chen, Y.T.
Isolated nucleic acid molecules encoding SSX family members and
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Isolated nucleic acid molecules encoding SSX family members and
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                                                                       ATGAACGGAGGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAAAG
                                                                                                                ATGAACGGAGACGACCTTTGCAAGGAGACCCAGGGATGATGTCCTCAAATATCAGAAG
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    2.6e-164;
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                          576; Conservative
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TITLE

RESULT

COMMENT

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/db_xref="g1:2952023"
/translation="mkGDDAPARRPRDDAQISEKLRKAFDDIAKYFSKKEWEKMKSSE
/translation="mkGDDAPARRPRDDAQISEKLRKAFDDIAKYFSKKEWEKMKSSE
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SLQRIFPRLIMPKKAPAEEBUGIJKEVPBASGPQNDGKQLCPPGNPSTLEKINKTSGPKRG
KHAWTHRLRERKQLVVYEBISDPEEDDE"
                                                                                                                                        PRI 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SSX4"
hote="corresponds to the 5' PCR primer that was used to
hote="corresponds and is identical to SSX2, Genbank
isolate this gene and is identical to SSX2, Genbank
Accession Number X86175; therefore, the SSX4 gene sequence
                                                                                                                                                                                                                                                                                                                              Gure, N.O., Tureci, O., Sahin, U., Tsang, S., Scanlan, M.J., Jager, E., Knuth, A., Pfreundschuh, M., Old, L.J. and Chen, Y.T. SSX: a multigene family with several members transcribed in normal testis and human cancer lint. J. Cancer 72 (6), 965-971 (1997)
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                                                                                                                                                                                                                                                                           Euteleostomi;
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/note="putative translation product; Kruppel-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 576)
Gure, A.O., Tureci,O., Sahin,U., Tsang,S., Scanlan,M., Knuth,A.
Pfreundschuh,M., Old,L.J. and Chen,Y.-T.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 576)
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100.0%; Pred. No. 2.6e-164;
ive 0; Mismatches 0;
    576
                                        576
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Submitted (05-FB1997) Pathology C-320,
York Ave., New York City, NY 10021, USA
Location/Qualifiers
                                                                                                                                      576 bp mRNA
mRNA, complete
    541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
                                      AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
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/organism="Homo sapiens"
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/product="SSX4"
/protein_id="AAC05820.1"
/db_xref="GI:2952023"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
1. .576
                                                                                                                                            Homo sapiens SSX4 (SSX4)
U90841
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PN JP 202519013-A/5
PD 02-JUL-2002
PP 25-JUN-1999 JP 2000557145
PR 26-JUN-1998 US 09/105839
PR 02LEM TURECI, UGUR SAHIN, MICHAREL PFREUNDSCHUH, GEORG RAMMENSEB, PI STEPAN STEVANOVIC, PAO TESIG CHEN ALI GURE, LLOYD J OLD PC C12N15/09, A61K38/00, C07H21/04, C12N5/10, C12P21/04, C12Q1/68, PC
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            Turecilo., Sahin,U., Pfreundschuh,M., Rammensee,G., Stevan Chen,Y.T., Gure,A. and Old,L.J.
SSX gene, method of determining the occurrence of cancer:
by determining the expression of peptides originating in gene and NY-ESO-1 gene and utilization thereof
LUDDWIG INSTITUTE FOR CANCER RESEARCH
DN HOROSIGHOR (human)
Pur 2002519013-A/5
DN UC-JUL-2002
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0; Mismatches 0;
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NY-ESO-1 gene and utilization
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/organism="Homo sapiens"
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_xref="taxon:9606"
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Best Local Similarity 100.
Matches 576; Conservative
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1250)

Strauberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schemer, C.M., Schuler, G.D.,
Altschul, S.F., Jordan, H., Morse, T., Mang, J., Hsieh, N.K.,
Hopkins, R.F., Jordan, H., Morse, T., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.M. B., Bonaldo, M.A., Peters, G.J.,
Abramson, R.D., Millahy, S.J., Boak, S.A., McEwant, F.L.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Millahy, S.J., Boaks, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wanny, D.M., Sodersen, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, A., Rodrigues, S.,
Banchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
buman and mouse odna Sci. U.S.A., 99 (26), 16899-16903 (2002)
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                                                                                                                                                                     TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCCAAGAAGCCAGCAGGAAGAA 360
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     CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240
                                                               GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAAACGTCCTCAGATGACT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens synovial sarcoma, X breakpoint 4, transcript variant 1, mRNA (cDNA clone MGC:12411 IMAGE:3961688), complete cds.
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Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u> AAACATGCCTGGACCCACAGACTGCGTGAGAAAAGCAGCTGGTGGTTTATGAAGAGATC</u>
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KEYWORDS
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NIH-MGC Project URL: http://mgc.nci.nih.gov

REMARK

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/db_xref="LocusID:6759"
/translation="MNGDDAPARRPENDAQISEKLRKAFDDIAKYFSKKEWEKMKSSE
/translation="MNGDDAPARRPENDAQISEKLRKAFDDIAKYFSKKEWEKMKSSE
ryvywkklnysvymyklgfkytlpppmkskraadfendfendruhernqverpomtrg
slorippkinpkkapabebanikkeybbasgpendskolcuppqnpstlekinktsgepkrg
KHAWTHRLRERKQLVVYEEISDPEEDDE"
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                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: m Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28559011.
Location/Qualifiers
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                                                                CDNA Library Preparation: CLONTBCH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codom_start=1
/prodouc="symovial sarcoma, X breakpoint 4, isoform a"
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/db_xref="GI:13529095"
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/note="KRAB; Region: krueppel associated box"
/db_xref="CDD:smart00349"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/mol_type="mRNA"
/clone="MGC:12411 IMAGE:3861688"
/tissue_type="Bladder, carcinoma"
/clone_lib="NIH MGC_53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 574.4; DB 9;
Pred. No. 8.8e-164;
0; Mismatches 1;
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/db_xref="LocusID:6759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="Vector: pDNR-LIB'
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity 99.8
Matches 575; Conservative
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Db 452 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGAAAGAGTGTGC 511 Qy 421 CCCCGGGAAATCCAAGTGCTTTGGAGAAGTTAACAAGAGAGCATCTGGACCCAAAAGGGGG 480	RESULT 11 AXB21947 LOCUS DEFINITION Sequence 75 from Patent W003068961. AXB21947 AXB21947 AXB21947 AXB21947 AXB21947 VERSION AXB2194 VERSION AXB21100 AXB21100 AXB21100 AXB21100 AXB21100 AXB21100 AXB21100 AXB21100 AXB2	1 TIGGGAGGAGGAGCCTTTGCAGGAGCCCAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA
Db 359 TTCGGCAGCTCCCAGAGAATCTTCCCGAAGAACCAAGAAGCCAGCAGAGGAAGAA 18 Qy 361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAATGATGGGAAACGCTGTGC 420 419 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAATGATGGGAAACCGTGTGC 478 Qy 421 CCCCCGCGAAATCCAGGGCGC 480 CCCCCGGGAAATCCAAGAGGCAACGCAGAAACGAGGGGG 480 CCCCGGGGAAATCCAAGAGAATCAACAGACACTGGACCCAAAAGGGGG 530 Q79 CCCCGGGAAATCCAAGAGAATCAACAGAGAGACTGGACCCAAAAGGGGG 530 Qy 481 AAACATGCCTGGACCCACAGACGCGGGGGTGCTTATTGAAGGGGG 530 Db 539 AAACATGCCTGGACCCACAGACTGCTGCAGAAAGGAGTC 540 CCCCGGGAACCCACAGACTGCTGCAGAAAGGAGTC CCCCGGGAAACCCACAGACTGCTGCAGAAAGCAGCTGGTGGTTTATGAAGAGATC 598 CCCCCAGGACCCACAGACTGCTGCAGAAAGCAGCTGCTGTTATGAAGAGATC 598 CCCCCAGGACCCACAGACTGCGTGAAAAGCAGCTGCTGCTTTATGAAGAGATC 598 CCCCCAGGACCCACAGACTGCGTGCTGCTGCTTTATGAAGAGATC 598 CCCCCACAGACTGCGTGCTGCTGCTTTATGAAGAGATC S98 CCCCCACAGACTGCGTGCTGCTGCTTTATGAAGAGATC S98 CCCCCACAGACTGCGTGCTGCTGCTTTATGAAGAGATC CCCCCACAGACTGCTGCTGCTGCTTTATGAAGAGATC CCCCCCACAGACTGCTGCTGCTGCTTTATGAAGAGAGTC CCCCCCACAGACTGCTGCTGCTGCTTTATGAAGAGAGTC CCCCCCACAGACTGCTGCTGCTGCTTTATGAAGAGAGTC CCCCCCACAGACTGCTGCTGCTGCTTTATGAAGAGAGTC CCCCCCCACAGACTGCTGCTGCTGCTTTATGAAGAGAGTC CCCCCCCACAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	OY 541 AGCGACCCTGAGGAAGATGACGTAACTCCCCTCG 576	Query Match 86.2%; Score 496.6; DB 6; Length 766; Best Local Similarity 91.5%; Pred. No. 4.6e-140; Matches 526; Conservative 0; Mismatches 49; Indels 0; Gaps 0; Andahacogaeaccaeacaeaccaeacaeacaeacaeacaeacaeaca

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Patent: US 5798264-A 2 25-AUG-1998;
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                                272 craderricaaddecaccerceacerricardraraaaaaddeceaadaerredag
                                                                GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                                                   TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGGAAGAA
                                                                                                                                                   361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                                                                                                                                     421 CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCCAAAAAGGGGG
                                                                                                                                                                                                                                                                                                       512 CCCCCGGGAAAACCAACTACCTCTGAGAATTCACGAGAGATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                                                                                     481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
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Sequence 2 from patent US 5798264.
AR025465
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1 (bases 1 to 931)
Pfreundschub, M.
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EHAWTHRLRERKQLYTYEZISDPEEDDE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coper, C.S.
Direct Submission
Submitted (10-APR-1995) C.S. Cooper, Institute of Cancer Research, Haddow Laboratories, Cotswold Road, Sutton, Surrey SM2 5NG, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
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       540
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                                   631
                                                                                                                                                                                                                                                                                                                                                Crew, A.J., Clark, J., Fisher, C., Gill, S., Grimer, R., Chand, A., Shipley, J., Gusterson, B.A. and Cooper, C.S.
Fusion of SYT to two genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel-associated box in human synovial sarcoma EMBO J. 14 (10), 2333-2340 (1995)
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                          481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAATC
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                                                                                                                                                                                        linear
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/gene="SSX2"
/note="Kruppel aaociated box homology"
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larity 91.5%; Pred. No. 4.6e-140;
Conservative 0; Mismatches 49;
                                                                     575
                                                                                                     mRNA
                                                                                                                                                                                                                                                          SSX1 gene; SSX2 gene; synovial sarcoma.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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/db_xref="G0A:015385"
/db_xref="SWISS-PROT:Q16385"
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R. sapiens mRNA for SSX2 protein.
X86175
X86175.1 GI:829113
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Db 459 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGGAAAGACTGTGC 518 Qy 421 CCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 480 Db 519 CCCCGGGAAAACCAACTCCTGAGAAGATTCACGAGAGATCTGGACCCAAAAGGGGG 578	Qy 481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAAGCAGCTGGTGGTTTATGAAGAGATC 540	Qy 541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575	RESULT 15 AR117874 LOCUS LOCUS DEFINITION Sequence 2 from patent US 6140464. VERSION AR117874 VERSION AR117874.1 GI:14098780	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 931) AUTHORS Pfreundschuh, M. and Rammensee, HG. TILLE Nonapeptides that bind a HLA-A2.1 molecule JOHENAL Patent: US 6140464-A 2 31-OCT-2000; FEATURES 1931 SOURCE //organism="unknown" ORIGIN	Query Match 86.2%; Score 496.6; DB 6; Length 931; Best Local Similarity 91.5%; Pred. No. 4.7e-140; Matches 526; Conservative 0; Mismatches 49; Indels 0; Gaps 0;	OY 1 ATGAACGGAGACGCCTTTGCAAGGAGCCCAGGGATGCTCAAATATCAGAGAAG 60	OY 61 TTACGAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGAAAGA	OY 121 AAATCCTCGGAQAAATCGTCTATGTGTATATGAAGGTAAAGTATGAGGTCATGAGGTCATAA 180	Oy 181 CTAGGITTCAAGGICACCTCCCACCTTTCATGGGGGGTGGAAACGGGCTGCAGACTTCCAC 240	QY 241 GGGAATGAITTTGGTAACGATCGAAACCACAGGAATGAGTTGAACGTCCTCAGATGACT 300	Qy 301 TICGGCAGCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAGAGACAGCAGCAGGAAGAA 360	QY 361 AATGGTITGAAGGAAGTGCCACAAGGCATCTGGCCCACAAATGATGGGAAACAGCTGTGC 420 DD 459 AATGATTCGGAGGAAGTGCCCAGAAGCATCTGGCCCACAAAATGATGGGAAAGAGCTGTGC 518	OY 421 CCCCGGGAAATCCAAGTACCTTGGAGAAAGATTAACAAGACACTTGGACCCAAAAGGGGG 480	OX 481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
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579 GAACATGCCTGGACCCACAGACTGCGTGAGAGAAACAGCTGGTGATTTATGAAGAGATC 638

541 AGCGACCCTGAGGAAGATGACGACTAACTCCCCTC 575

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Title:

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Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

		Description	844	Abg83858 Human SSX		Aav70060 Human SSX	Aat11780 Human X-c	Abs73282 DNA encod	Aad54033 Human col	Abg83844 Human SSX	_		Aat47748 Melanoma	Aav04267 Melanoma	Abl64122 Breast ca	Abl63730 Breast ca	Aas80402 DNA encod	Aas80399 DNA encod	Aav70061 Human SSX	Aat11779 Human X-c	Aat11781 Human SYT	Aat11782 Human SYT	Aas80401 DNA encod	Aas80404 DNA encod	Abs73281 DNA encod
SUMMARIES	;	ID	- 24	ABQ83858	ADC09598	AAV70060	AAT11780	ABS73282	AAD54033	ABQ83844	ADC09570	ADD25523	AAT47748	AAV04267	ABL64122	ABL63730	AAS80402	AAS80399	AAV70061	AAT11779	AAT11781	AAT11782	AAS80401	AAS80404	ABS73281
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ALIGNMENTS

ABK84472 standard; cDNA; 576 ABK8447

BP.

(first entry) 14-AUG-2002 Human cDNA differentially expressed in granulocytic cells #1043.

Human; ss, granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; andlt respiratory distress syndrome; inflammatory bowel disease; Crohm's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

Homo sapiens

WO200228999-A2.

11-APR-2002.

03-OCT-2001; 2001WO-US030821.

03-OCT-2000; 2000US-0237189P.

(GENE-) GENE LOGIC INC.

Vockley J; Yamaga S, Weissman SM, Beazer-Barclay Y,

WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

claim 1; SEQ ID NO 1043; 114pp; English.

The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by NMA chip analysis a sgiven in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are

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modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression at tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating of expression of the gene is indicative of inflammation with an employer, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue, having inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for modulating GA, M3 is useful conflammatory disease, by contacting a tissue having inflammation of a uniflammation in a tissue, M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation of separation in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation disease (e.g. cardiac reperfusion injury, renal reperfusion injury, ARDS, adult conflammatory disease, ulceration of disease, ulceration of disease, ulceration of disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC
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The present invention describes an isolated epitope (1) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition (VC) comprising (1). (1) has vaccine or immunotherapeutic composition treating an animal, by administering to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic composition. W is also useful for evaluating administering VC to an HLA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (1) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises ELISPOT analysis, limiting dilution analysis, flow cytometry, in situ hybridisation and/or polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to ABP747;3 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09
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                                                                                                                                                                                                                                                epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 576 BP; 187 A; 127 C; 150 G; 112 T; 0 U; 0 Other;
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                             541 AGGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
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100.0%; Pred. No. 9.3
ive 0; Mismatches
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                                                                                                                                                                                                              Human SSX-4 encoding cDNA SEQ ID NO:599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 185; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CTLI-) CTL IMMUNOTHERAPIES CORP
                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2001; 2001US-0282211P.
07-NOV-2001; 2001US-0337017P.
07-MAR-2002; 2002US-0363210P.
                                                                                                               ABQ83858 standard; cDNA; 576
                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2002; 2002WO-US011101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%;
Conservative
                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                WO200281646-A2,
                                                                                                                                                                                                                                                                                                Homo sapiens.
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Matches 576;
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epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemotherapy. blochemotherapy or surgery. The composition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC -peptide complexes of the invention are useful for determining specific T call frequency. This method is useful for evaluating immunological response, by performing the method prior to and subsequent to an immunological immunisation step. Compositions of the invention are useful for diagnosing a disease. The current sequence represents an epitope of the
                                                                                                                                                                                                                                                                                                                               AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                        , Score 576; DB 9; Length 1250;
, Pred. No. 1.4e-171;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                             Sequence 1250 BP; 373 A; 302 C; 278 G; 297 T; 0 U; 0 Other;
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                                                                                                                                                              diagnosing a disease. The current sequence re
invention with high affinity for MHC class I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epitope having high affinity for major histocompatibility complex class useful for treating an animal, evaluating immunogenicity of a vaccine or therapeutic composition and for diagnosing a disease.
                                                                                 The invention relates to an isolated epitope polypeptide that has high affinity for major histocompatibility complex (MHC) class I, and an
                               AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAAACTATGAGGTCATGACTAAA
                                                                                                                                                                                                                     TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAAGAAGAA
AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
                                                               CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
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major histocompatibility complex class I; MHC class I;
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2001US-0337017P.
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481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; SSXZ gene; synovial sarcoma; X-chromosome; breakpoint-2; contithine-delta-aminotransferase; OATLZ gene; XP11.2; SSXI gene; translocation; chromosome-18; 18q11.2; SYT gene; gene fusion, SYT-SSXZ; fusion protein; primer; PCR; polymerase chain reaction; Smal; LpsI; probe; antibody; monoclonal antibody; hybridisation; antiense; antitumour; recombinant vaccine; vaccinia virus; vector; cancer; diagnosis; therapy; sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing synovial sarcoma by detection of e.g. SYT and SSX1 sequences, based on X18 trans-location - by amplification of trans-location sequences or detection of the encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents the SSX2 gene (synovial sarcoma X-chromosome breakpoint-2). The gene is at the location of a breakpoint at Xp11.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= f
/note= "3'-Region present in SYT-SSX2 fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= e
/note= "Breakpoint for SYT translocation"
                                                                                                    AGCGACCTGAGGAGGATGACGAGTAACTCCCTCG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                '*tag= g
'note= "Binds primer AAT11784"
                                                       AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aa:Ser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aa:Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/codon= seq:TTC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '*tag= b
'codon= Beq:AAG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon= seq:GAG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= d
/codon= seq:CGT,
                                                                                                                                                                                                                                                 BP
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                                                                                                                                                                                                                                              AAT11780 standard; cDNA; 766
                                                                                                                                                                                                                                                                                                                                                                                                                      Human X-chromosome SSX2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-GB001704
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                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference 257. .259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377. .379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gusterson
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P-PSDB; AAR90677.
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                                                                                                                                                                                                                                                                                                                                                              16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996
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                                                                                                       541
                                                                                                                                                                                                                                                                                                      AAT11780;
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LU AAT1780

LU AAT1780

LO AAT1780

XXX AAT1

XXX AAT1

XXX Huma

XXX Huma

XXX Huma

XXX Homo

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of a newly isolated human SSX4 cDNA clone. The cDNA was isolated from a human testicular cDNA by PCR amplification using primers (see AAV7006-63) based on the known SSX2 sequence. A SSX5 clone (see AAV70061) was also obtained. 2 Forms of SSX4 were identified. One of these lacked nucleotides 331-466 but was otherwise identical to the present SSX4 sequence and is described as an alternatively spliced form. SSX4 shares 89.4% homology to SSX1 on the nucleotide level and 79.3% at the amino acid level. The inventional additionally provides expression vectors, transformed or transfected cells that can be used to produce SSX proceins, and primers (see AAV70062-73) useful for determining expression of an SSX gene in a sample. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCCCGGGAAATCCAAGTACCTTGGAGATTAACAAGACATCTGGACCAAAAGGGGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTACGAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGAAAAGAGAAAAAGATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATCCTCGGAGAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAGGITTCAAGGICACCTCCCACCTTTCAIGCGIAGIAAACGGGGCTGCAGACTTCCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         craderircaadercaccriccaccrircareceracraaaceeecrecaeacriccae 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGAGAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCAAAAATGATGGAAAACAGCTGTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             New SSX gene family members - useful for assaying for cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSX genes can be used to assay for cancers such as melanoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                      Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 574.4; DB 2;
Pred. No. 3e-171;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                      O, Sahin U, Tsang S,
Old LJ, Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 12; 19pp; English
                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998~610379/51
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                                                                                                                                                                                                                                                                                                      Gure AO, Tureci
Pfreundschuh M,
                       WO9850528-A1
                                                                                                                                 25-FEB-1998;
                                                                                                                                                                                         05-MAY-1997;
                                                                         12-NOV-1998
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90 A9

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HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NFL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;

rhabdomyosarcoma; synovial sarcoma; viral infection; gene;

WO200269900-A2 Homo sapiens

12-SEP-2002

(CONF-) CONFORMA THERAPEUTICS 01-MAR-2001; 2001US-0272751P. 01-MAR-2002; 2002WO-US006518

Burrows FJ;

Fritz LC,

WPI; 2002-698710/75. P-PSDB; ABG95081

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420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATCCTCGGAGAAAATCGTCTATGTGTATGAAGCTAAACTATGAGGTCATGACTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAGGITICAAGGICACCCICCCACCTITCAIGCGIAGTAAACGGGCIGCAGACTICCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAGGTTTCAAGGCCACCTCCCACCTTTCATGTATAAACGGGCCGAAGACTTCCAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGAGGAAGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAACGGAGACGACGCCTTTGCAAGGAGACCCACGGTTGGTGCTCAAATACCAGAGAAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the translocation t(X;18) (p11.2;q11.2) found in human synovial sarcomas, two large joining of the SYT gene (AAT11778) on chromosome-18 at 18q11.2 to SXX2. The gene fusion is then transcribed to produce an SYT-SSX2 (AAT11781) fusion transcribt and translated into a fusion protein. SSX2 with Small and istinguished from related sequence SXX1 (AAT11779) by digestion with Smal and Lep1. Primer AAT11794 has been used in polymerase chain reaction amplification of SXX2 sequences. Detection of the gene or its product in an abnormal location or as a fusion may be used in diagnosis of synovial sarrowa, using primers, probes, humanised antibodies, may also be used therapeutically, and antitumour recombinant vaccines may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u> AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCCACAAAATGATGGGAAAGAGCTGTGC</u>
                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAACGGAGACGACCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTIGETITIGAAGGAAGTGCCAGAGGCCATCTGGCCCACAAAATGATGGAAACAGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCAAAAAGGGGG
                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                       Length 766;
                                                                                                                                                                                                                                                                                 Sequence 766 BP; 229 A; 181 C; 200 G; 156 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                         Score 496.6; DB 2;
Pred. No. 1.5e-146;
within an ornithine-delta-aminotransferase OATL2
                                                                                                                                                                                                                                           constructed e.g. in a vaccinia virus vector
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                         86.2%;
91.5%;
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 526; Conserv
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (1), treating cancerous cells containing (1) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with foromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in theorogeneous cell population, treating proliferative disease (e.g. rhematoid atthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein or cellular protein isoform in patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoletch disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), ABL, AML, AML, AML, and CML, ó 120 240 211 180 271 92 argaacgagacgacgccrrrdcaaggagacccacggrrgcrgcrcaaaraccagagaag 151 craegrircaageccacecreecercrireargranaaaceceaagacriecag 331 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90. or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Bwing's sarcoma, melanoma, libosarcoma, rabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This represents the DNA sequence of a chromosome aberration 1 ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAG 152 Arccaragecerregargararreceaarracerreceaagegagagagagagarg AAATCCTCGGAGAAAATCGTCTATGTGTATGAAGCTAAACTATGAGGTCATGACTAAA AAAGCCTCGGAGAAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAAA CTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC Gaps ; 0 Length 766; 766 BP; 229 A; 181 C; 200 G; 156 T; 0 U; 0 Other; Indels 49; DB 6; Query Match 86.2%; Score 496.6; DB 6; Best Local Similarity 91.5%; Pred. No. 1.5e-146; Matches 526; Conservative 0; Mismatches 49; Disclosure; Page 236; 389pp; English 61 212 Sequence 121 181 ð g ð qq à g à q

571

481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540

512

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GAACATGCCTGGACCCACAGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAGATC 631

541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC

632

g

ABS73282 standard; DNA; 766

RESULT

Chromosome aberration, oncogenic fusion protein; cancer, proliferative disease; cellular protein isoform; heat shock protein 90;

DNA encoding human translocation (X; 18) (p11.2; q11.2) protein #2.

(first entry)

04-DEC-2002

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Length 766; Indels 180

211

271 240

120

151

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360

391

451 420 511 480 571 540 631

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331

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vaccine; immunotherapeutic; cytostatic; immunogenicity;
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                                                                                            Arccaaaadgccrrcgargararricccaaaracrrcrcraaggaagagrggaaaaagarg
                                                                                                                                                                                                       AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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                                                                   1 ATGAACGGAGACGACGTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAAG
 DB 7;
Score 496.6; DB 7;
Pred. No. 1.5e-146;
0; Mismatches 49;
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2001US-0337017P.
2002US-0363210P.
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86.2%;
91.5%;
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                  Similarity 91.5
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07-NOV-2001;
07-MAR-2002;
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                                  526;
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   GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCTCAGATGACT 300
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associated polypeptides as antigens that elicit immune response in colon
                                  GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                      TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGGAGGAGGAAGAA
                                                                                            AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                               CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                             CCCCCGGGAAAACCAACTACCTCTGAGAATTCACGAGAGATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                             AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer-associated polypeptide; immune response; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                   immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (I) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises ELISPOT analysis, limiting dilution analysis, flow cytomeerry, in situ hybridisation and/or polymerase chain reaction (PCR). ABD03843 to ABD038958 and ABP74128 to ABP74713 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                            represent sequences used in the exemplification of the present
                                                                                                                                             The present invention describes an isolated epitope (I) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition (VC) comprising (I). (I) has cytostatic activity. VC is useful for treating an animal, by administering to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic composition, by administering VC to an HLA-transgenic animal and evaluating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
                                                      Novel epitopes useful as vaccines, comprises peptides or nucleic acid encoding the peptides, that are useful epitopes of target-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.2%; Score 496.6; DB 7; Best Local Similarity 91.5%; Pred. No. 1.5e-146; Matches 526; Conservative 0; Mismatches 49;
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                                                                                                                 Claim 1; Page 148; 352pp; English.
            2003-067518/06.
                            P-PSDB; ABP74130
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The invention relates to an isolated epitope polypeptide that has high effinity for major histocompatibility complex (MHC) class I, and an epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemcherapy or biochemotherapy or surgery. The composition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC repeptide complexes of the invention are useful for determining specific T cell frequency. This method is useful for evaluating immunological response, by performing the method prior to and subsequent to an immunisation step. Compositions of the invention are useful for disease. The current sequence represents an epitope of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Epitope having high affinity for major histocompatibility complex class luseful for treating an animal, evaluating immunogenicity of a vaccine or therapeutic composition and for diagnosing a disease.
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major histocompatibility complex class I; MHC class I; cancer;
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91.5%; Pred. No. 1.5e-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention with high affinity for MHC class I.
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2002US-0363210P.
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standard; cDNA;
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Best Local Similarity
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07-MAR-2002;
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                                                              ADC09570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Melanoma; tumour antigen; HOM-MEL 40; serological fishing; vaccine; ds.
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             Length 766;
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                                 Pred. No. 1.5e-146;
0; Mismatches 49;
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               DB
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               Score 496.6;
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               86.2%;
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Matches 526, Conservative
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10-MAY-1996;
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                                                                                                                                                                                   420
                                                                                                                                                                                                                                                                                                                                     481 AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTTATGAAGAGTC 540
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CTAGGTTTCAAGGCCACCCTCCCACCTTTCATGTAATAAACGGGCCGAAGACTTCCAG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                          TTCGGCAGCCTCCAGAGATCTTCCCGGAGGATCATGCCCAAGAAGCCAGCAGAGGAAGAA
                                   GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                                                                                                     AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCAAAATGATGGAGGGAAACAGCTGTGC
                                                                    GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding domain-immunoglobulin fusion protein-associated DNA #46
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2002US-00053530.
2002US-0385691P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD25523 standard; DNA; 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-801317/75.
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ADD25523
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480

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molecules

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Novel method of serological fishing - allows isolation of molecule antigens) associated with pathological conditions, e.g. Hodgkin's disease, cancer or auto:immune disease.
                                             Claim 31; Page 29; 44pp; English
     WPI; 1997-051896/05
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designated HOM-MEL 40. It was isolated using a novel method in which a designated HOM-MEL 40. It was isolated using a novel method in which a cDNA library prepol from malignant melanoma and expressed in B. coli colls. Lysates of the host cells and with sera that had been treated to remove interfering binding partners. This involved contacting the sample with lysates of untransfected host cells and with host cells transformed with the same vector (phage lambda) used to make the CDNA library. The method, termed serological fishing, can be used to detect antigens in human tissues, esp. tumour cells, which are useful in the moliganosis of diseases and/or for immunotherapy and gene therapy of infectious, autoimmune and malignant diseases (see also AAA-4747-49). HOM-MEL 40 is expressed in 50% of melanomas, 20% of prostate cancers, 20% of gastric cancers, 20% of colorectal cancers, 12% of lung cancers and calls present a nonomer (see also AAW-09449- 52) derived from HOM-MEL, suggesting that HOM-MEL 40-specific vaccines, useful in inducing T lymphocytes, are possible

Sequence 931 BP; 274 A; 207 C; 231 G; 219 T; 0 U; 0 Other;

360 458 578 638 420 518 480 398 159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG 218 219 AAAGCCTCGGAGAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGCTATGACTAAA 278 240 cracerricaacccacccrccaccrrrcarcraraaaaccccaaccarcracae 338 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300 ATGAACGGAGACGACGCCTTTGCAAGGAGCCCACGGTTGGTGCTCAAATACCAGAGAAG 158 AAACATGCCTGGACCCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGGAGATC 1 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAG AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA CTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGTTCCAC GGGAATGATTTGGATGATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT TTCGGCAGCCTCCAGAGATCTTCCCGGAGGTCATGCCCAAGAAGCCAGGAGGAAGAA AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGAAACAGCTGTGC AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGGAAAGAGCTGTGC CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG cecededadadecraecreererendadarreacadadareredadaece GAACATGCCTGGACCCACAGACTGCGTGAGAAAAACAGCTGGTGATTTATGAAGAGATC Gaps . 0 86.2%; Score 496.6; DB 2; Length 931; larity 91.5%; Pred. No. 1.6e-146; Conservative 0; Mismatches 49; Indels 0 575 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC Local Similarity les 526; Conserv 519 279 301 399 361 459 421 481 541 241 339 121 181 Query Match Matches qq ò g δ g 8 à g Д ò g δ 셤 à g δ a ð

120 218 180 278

159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGGGGGGAAAAGATG 121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA CTAGGITICAAGGICACCCICCCACCITICAIGCGIAGIAAACGGGGCIGCAGACITCCAC 240

AAAGCCTCGGAGAAAATCTTCTATGTGTATTGAAGAAAAGTATGAGGCTATGACTAAA

219 181

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639 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC

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clone HOW-MEL-40 was isolated from a human malignant melanoma oDNA-
library using a method, designated serological fishing, designed to
cldentify immunoracity markers of disease. In this method, cells
contracteristic of a disease are used to prepare a cDNA library for
characteristic of a disease are used to prepare a cDNA library for
characteristic of eukaryotic or prokaryotic cells, and the cells grown to
creative with these cells, then the stripped sample is similarly treated
contracted with lysate of the library cells, so that specific components
incubated with lysate of the library cells, so that specific components
in the sample may bind to the expression protein. Proteins that form
complexes are identified as disease markers. In the case of HOM-
mEL-40, the new melanoma associated antigen is strongly expressed in
complexed antigon is strongly expressed in
complexed at the complexed antigon is strongly expressed in
complexed at the confident of the case of HOM-
melanoma, but not healthy tissues. The deduced amino acid sequence
conclusional fishing method was also used to identify a claimed
con marker (see AAV04262) of Hodgkin's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mucleic acid and derived protein are markers for Hodgkin's disease - used in identifying immuno:reactive markers of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAACGGAGGCGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAAATATCAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCACGGTTGGTGCTCAAATACCAGAGAAG
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                                                                                                                                                                marker; antigen; diagnosis; serological fishing; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.2%; Score 496.6; DB 2;
llarity 91.5%; Pred. No. 1.6e-146;
Conservative 0; Mismatches 49;
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                                                                                                                             Melanoma antigen clone HOM-MEL-40.
               AAV04267 standard; cDNA; 931 BP
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                                                                                         (first entry)
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nes 526; Conserv
                                                                                                                                                                                      HOM-MEL-40; ss.
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                                                     AAV04267;
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AAV04267
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121 AAATCCTCGGAGAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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Best Local Similarity 91.5
Matches 526; Conservative
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                                                                       CTAGGTTTCAAGGCCACCCTCCCACCTTTCATGTAATAAACGGGCCGAAGACTTCCAG 338
                  GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
                                                                                                                                                                                                                                                                                                                                               Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                  GAACATGCCTGGACCCACAGACTGCGTGAGAAAACAGCTGGTTTATGAAGAGATC
                                    GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
                                                                                                             AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCCACAAAATGATGGAAAGAAGCTGTGC
                                                       TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGAAAA
                                                                                           AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                 CCCCCGGGAAAACCAACTACCTCTGAGAAGATTCACGAGAGATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                                                                              Breast cancer related gene sequence SEQ ID NO:2459.
                                                                                                                                                                                                        AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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25-SEP-2000; 2000US-0234923P.
25-SEP-2000; 2000US-0234924P.
25-SEP-2000; 2000US-0235077P.
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2000US-0235077P.
2000US-0235082P.
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2000US-0235638P.
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2000US-0233133P.
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05-JUN-2000; 2
18-SEP-2000; 2
18-SEP-2000; 2
20-SEP-2000; 2
20-SEP-2000; 2
20-SEP-2000; 2
22-SEP-2000; 2
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25-SEP-2000;
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26-SEP-2000;
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The present invention describes a method (MI) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent cobe tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in dicative of anti-neoplastic activity. (I) has cytostatic expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an enti-neoplastic agent, and can be used for producing a product which is anti-neoplastic agent, and can be used for producing a product which is comparate of the agent. MI can be used in the treatment of cancer such to properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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2000US-0236034P.
2000US-0236109P.
2000US-0236111P.
2000US-0236812P.
2000US-0237172P.
2000US-0237278P.
2000US-0237294P.
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2000US-0237604P.
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2000US-0244867P.
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Weaver Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-188264/24.
                                                                                                                                                              29-SEP-2000; 29-SEP-2000; 20-0CT-2000; 20-0C
     28-SEP-2000;
28-SEP-2000;
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Gaps

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Indels

Length 1309;

DB 6; 49;

86.2%; Score 496.6; DB 6; 91.5%; Pred. No. 1.9e-146;

Mismatches

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1 ATGAACGGAGGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAAATATCAGAGAAG

AAAGCCTCGGAGAAATCTTCTATGTGTATATGAAGAGAAAGTATGAGGTTATGACTATGACTAAA 278 CTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240 cragerincaadeccaccriccaccinicardrafaraaaadeccaaadacriccag 338

219 181 279

2000US-0235711P.

2000US-0235720P 2000US-0235840P 2000US-0235863P 2000US-0236028P 2000US-0236032P

27-SEP-2000;

28-SEP-2000;

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Horrigan

Endress G,

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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent copplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in air least 95% identical to (S), where a change in comprises in indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is cantinoplastic agent. M1 can be used in the treatment of cancer such to make a set of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarionem, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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28-SEP-2000; 2000US-0236109P.
29-SEP-2000; 2000US-0236111P.
29-SEP-2000; 2000US-0236842P.
29-SEP-2000; 2000US-0236842P.
02-OCT-2000; 2000US-0237172P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237294P.
02-OCT-2000; 2000US-0237296P.
03-OCT-2000; 2000US-0237456P.
03-OCT-2000; 2000US-0237598P.
03-OCT-2000; 2000US-0237604P.
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01-NOV-2000; 2000US-0244667P.
01-NOV-2000; 2000US-024667P.
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Weaver Z;
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         GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT
                                                 GGGAATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT
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polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
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84.6%; Score 487.2; DB 5;
Best Local Similarity 91.3%; Pred. No. 1.6e-143;
Matches 528; Conservative 0; Mismatches 48;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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	ence of Cancer	3; Length 576; 184; Indela Gardardcrcaarr GATGATGATGATGATGATGATGATGATGATGATGATGATG
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ω ω α γ α α α α α α α α α α α α α α α α α	ULT 1 09-105-839D-5 equence 5, Application US/09105839D atchn No. 628776 APPLICANT: Tureci, Ozlem APPLICANT: Tureci, Ozlem APPLICANT: Chen, Yao-Tseng APPLICANT: Sahin, Ugur APPLICANT: Old, Lloyd J APPLICANT: Pfreundschuh, Michael TITLE OF INVENTION: Method for Dete TITLE OF INVENTION: Expression of FILE REFERRNCE: LUD 5556 CURRENT APPLICATION NUMBER: US/09/1	CURRENT FILING DATE: 1998-06-1 PRIOR APPLICATION NUMBER: US 0 PRIOR FILING DATE: 1997-05-05 NUMBER OF SEQ ID NOS: 72 LEQ ID NO 5 LEQ ID NO 6 TYPE: DNA CORGANISM: Homo sapiens 09-105-839D-5 Leary Match Local Similarity 100.0%; lest Local Similarity 100.0%; lest Local Similarity 100.0%; latches 576; Conservative 1 ATGAACGCAGACGCCT 1 ATGAACGCAGACGCCT 1 TACGAAAGCCCTTCGATG 11
© 4 € € € € € € € € € € € € € € € € € €	SULT 1 -09-105-839D-5 Sequence 5, Applica Parent No. 6287766 GENERAL INFORMATION APPLICANT: Chen, TITLE OF INVENTION FILE REFERENCE: LU CURRENT APPLICANTO CURRENT APPLICANTO	'FIL TPLI TPLI 1 57 1 57 839D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT: Scanlan, Matthew J.; Knuth Alexander; Pfreundschuh, Michael; Old,
APPLICANT: Libyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Family
TITLE OF INVENTION: Family
MUMBER OF INVENTION: Members And Uses Thereof
CORRESPONDENCE: 14
CORRESPONDENCE: 14
ADDRESSE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
                                                                                                                                                                            GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                                           AAATCCTCGGAGAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/796,780
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/851,138
FILING DATE: 5-May-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09796780; Patent No. 6339140
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TELEFAX: (212) 752-558
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08851138C
Patent No. 6291658
GENERAL INFORMATION:
APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
APPLICANT: Garalan, Matthow J.; Knuth Alexander; Pfreundschuh, Michael; Old, APPLICANT: Lloyd J.; Chen, Yao-Tseng
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX Family
TITLE OF INVENTION: Members And Uses Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
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100.0%; Pred. No. 1.7e-184;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,138C
FILING DATE: 5-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: LUD 5480
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hanson, No. 6291658man D. REGISTRATION NUMBER: 30,946
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS
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Best Local Similarity 100.'
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US-08-851-138C-1
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PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1998-06-26
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                                                                                                         Length 576;
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                                                                                                    Score 576; DB 4; L
Pred. No. 1.7e-184;
0; Mismatches 0;
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; GENERAL INFORMATION:
                                                                                                 100.0%;
ilarity 100.0%;
Conservative 0;
     ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-344-040C-5
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Best Local Similarity
Matches 576; Conserv
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APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Bamensee, Hans Georg
APPLICANT: Ramensee, Hans Georg
APPLICANT: Ramensee, Hans Georg
APPLICANT: Remensee, Hans Georg
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
TITLE OF INVENTION: Gene, and Uses Thereof
TITLE OF INVENTION: Bayer
CURRENT APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 5
LENGTH: 576
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100.0%; Pred. No. 1.7e-184;
ive 0; Mismatches 0;
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                                                                                                      Query Match
Best Local Similarity 100.
nucleic acid
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GENERAL INFORMATION:
                         STRANDEDNESS:
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TOPOLOGY:
US-09-796-780-1
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US-09-344-040C-5
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Pred. No. 1.7e-184;

Mismatches

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CTAGGTTTCAAGGTCACCCTCCCACTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240
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                                       Score 576; DB 4; L Pred. No. 1.7e-184;
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APPLICANT: Gure, Ali O.
APPLICANT: Gure, Ali O.
APPLICANT: Gure, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Cancer Associated Antigens and
TITLE OF INVENTION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
BARLIER APPLICATION NUMBER: PCT/US98/14679
BARLIER FILING DATE: 1998-07-15
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                             Mismatches
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                                   Query Match
Best Local Similarity 100.0%; Pr
Matches 576; Conservative 0;
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ORGANISM: Homo sapiens
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                                              CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCCAAAAGGGGG
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| GENERAL INFORMATION:
| APPLICANT: Scanlar, Matthew J. APPLICANT: Scanlar, Matthew J. APPLICANT: Scanlar, Matthew J. APPLICANT: Gure, Ali O. APPLICANT: Williamson, Barbara APPLICANT: Chen, Yao-Tseng APPLICANT: Chen, Yao-Tseng APPLICANT: Old, Lloyd J. TITLE OF INVENTION: Therefor TITLE OF INVENTION: Therefor FILE REFERENCE: L0461/7062 CURRENT APPLICATION NUMBER: US/09/392,714A CURRENT FILING DATE: 1999-09-09 EARLIER APPLICATION NUMBER: PCT/US98/14679 EARLIER FILING DATE: 1998-07-15 NUMBER OF SEQ ID NOS: 30 | SEQ ID NO 16 | SEQ ID NO 16 | LENGTH: 766
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                                                                                                                                                                                                                                                                                                              AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG 576
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Query Match

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APPLICANT: Pfreundschuh, Michael
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                           Score 496.6; DB 1;
Pred, No. 1.5e-157;
0; Mismatches 49;
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VS-08-761-119-2
'Sequence 2, Application US/08761119
'; Patent No. 5798264
                      LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
                                                                                                                                                           tch 86.2%; al Similarity 91.5%; 526; Conservative C
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
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                                              ATGAACGGAGGCGCTTTGCAAGGAGACCCACGGTTGGTGCTCAAATACCAGAGAAG
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Patent No.. 5698396
GENERAL INFORMATION:
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
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REFERBNCE/DOCKET NUMBER: LUD 5410
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5698396ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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US-08-479-328-2
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ATGAACGGAGGACGACGTTTGCAAGGAGACCCACGGTTGGTGCTCAAATACCAGAGAAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
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                                                                                                                               NAME: Hanson, No. 5798264man D. REGISTRATION NUMBER: 30,946
REPERENCE/DOCKET NUMBER: LUD 5410.3
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (212) 688-9200
  APPLICATION NUMBER: US/08/761,119
                  FILING DATE: 6-DECEMBER-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double-stranded
                6-DECEMBER-1996
                                                                                                                                                                                                          TELEPHONE: (212) 688-920
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
IENGTH: 931, base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 91.5
Matches 526; Conservative
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                        US-08-761-119-2
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APPLICANT: Pfreundschuh, Michael TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And

Sequence 2, Application US/08668128B Patent No. 5840568

RESULT 10 US-08-668-128B-2

GENERAL INFORMATION:

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241 GGGAATGATTTTGGTAACGATCGAAACCACGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 AAAGCCTCGGAGAAAACCTTCTATGTGTATGAAGAAAAGTATGAGGCTATGACTAAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAGGTTTCAAGGTCACCCTCCCACCTTCCATGCGTAAAAGGGGCTGCAGACTTCCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIAGGITTCAAGGCCACCTCCCACCTTCAAGTGTAATAAACGGGCCGAAGACTTCCAG 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 496.6; DB 2;
Pred. No. 1.5e-157;
0; Mismatches 49;
                                                                                                                                                                                                                                             SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,128B
FILING DATE: 21-UWB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hanson, No. 5840568man D.
REGISTRATION NUMBER: 30,946
REGISCHENCE/DOCKET NUMBER: LUD 5441
TELECOMMUNICATION INFORMATION:
TELEPRA: (212) 688-9200
TELEPRA: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30,946
RR: LUD 5441
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/644,116
FILING DATE: 10-MAY-1996
PRICR APPLICATION NUMBER: 08/580,980
FILING DATE: 03-JANURRY-1996
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUN8-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.5%;
Matches 526; Conservative
                                             Felfe & Lynch
                                                                  805 Third Avenue
                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS
NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                     CITY: New York City
STATE: New York
ZIP: 10022
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                                             ADDRESSEE:
STREET: 80
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US-08-668-128B-2
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159 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGAGGAAAAAGATG 218
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                                                                                      219 AAAGCCTCGGAGAAATCTTCTATGTATATGAAGAGAAAGTATGAGGCTATGACTAAA
                                                                                                                                         181 CTAGGITTCAAGGICACCCICCCACCTTTCATGCGIAGIAAACGGGCTGCAGACTTCCAC
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                                                                                                                                                                                                                                                                                 339 gegaardartregaraardacceraacceregaarcagerreaacerecreagardacr
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Patent No. 6017716
GENERAL INFORMATION:
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: And Molecules Identified Thereby
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639 AGCGACCTGAGGAAGATGACGAGTAACTCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hanson, No. 6017716man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 5410.1
TELECOMUNICATION INPORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08/580,980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-CANUARY 1996
APPLICATION NUMBER: 08/479,3;
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-959-625-2
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       CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG 480
                                                                                                  481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC 540
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                                                 519 CCCCCGGGAAAACCAACTACCTCTGAGAAGATTCACGAGAGATCTGGACCCAAAAGGGGG
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TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 THIR'd Avenue
CITY: New York City
STATE: New York
ZIP: 100.22
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
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Pred. No. 1.5e-157;
0; Mismatches 49;
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA: 08/668,128
FILING DATE: 21-JUNE-1996
APPLICATION NUMBER: 08/644,116
FILING DATE: 21-JUNE-1996
APPLICATION NUMBER: 08/644,116
FILING DATE: 10-MAY-1996
PRIOR APPLICATION DATA: 1996
PRIOR APPLICATION DATA: 1996
FILING DATE: 03-JANUARY-1996
FILING DATE: 03-JANUARY-1996
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 3864015man D. REGISTRATION NUMBER: 30,946
FEFERENCE/DOCKET NUMBER: 30,946
FEFERENCE/DOCKET NUMBER: 1LUD 5441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 838-3884
INFORMATION FOR SEG ID NO: 2:
LENGTH: 931 base pairs
ILENGTH: 931 base pairs
STERANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,445
FILING DATE: 04-AUG-1997
                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08905445 Patent No. 5864015 GENERAL INFORMATION:
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nilarity 91.5%;
Conservative 0,
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Matches 526; Conserv
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US-08-905-445-2
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TOPOLOGY: linear
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                                                                                                                                             1 ATGAACGGAGACGACGTTTGCAAGGACCCAGGGATGATGCTCAAATATCAGAGAAG
                                                                                                                 Gaps
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TITLE OF INVENTION: Method For Identifying Or Isolating A Molecule
TITLE OF INVENTION: Method For Identified Thereby
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York City
ZIP: 10022
                                                                                                                 0
                                                                                     Length 931;
                                                                                                                 Indels
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                                                                                    Score 496.6; DB 3;
Pred. No. 1.5e-157;
0; Mismatches 49;
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OPERATING SYSTEM: PC-DOS
SOSTWARE: WORDERFECT
APPLICATION DATA:
APPLICATION NUMBER: US/09/008,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09008466 Patent No. 6020134 GENERAL INFORMATION:
LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
                                                                                  86.2%;
ilarity 91.5%;
Conservative
                                              linear
                                                                                                  al Similarity
526; Conserv
                                       TOPOLOGY:
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US-09-008-466-2
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US-08-959-625-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
86.2%; Score 496.6; DB 3
Best Local Similarity 91.5%; Pred. No. 1.5e-157
Matches 526; Conservative 0; Mismatches 49
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                                                                                                                                                                             NAME: Hanson, No. 6020134man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10,946
REFERENCE/DOCKET NUMBER: 10,5410.1
TELECOMONICATION INFORMATION:
TELECAX: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 931 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: Gouble-Etranded
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US-08-580-980A-2
; Sequence 2, Application US/08580980A
; Patent No. 6055191
; GENERAL INFORMATION:
; APPLICANT: Pfreundschuh, Michael
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,980
                                                                          FILING DATE: 03-JANUARY-1996
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
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                       638
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579 GAACATGCCTGGACCCACAGACTGCGTGAGAAAAAAAAGGGCTGGTGATTTATGAGAGATC
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                                                                                                                                                                                                                                                                                  APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Method For Identifying Or Isolating
TITLE OF INVENTION: A Molecule And Molecules Identified Thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 496.6; DB 3;
Pred. No. 1.5e-157;
0; Mismatches 49;
                                                                                                              639 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC
                                                                       541 AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,980
FILING DATE: 03-JANUARY-1996
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6103873man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10D 5410
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 931 base pairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                        ; Sequence 2, Application US/09053453; Patent No. 6103873; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.2%;
Best Local Similarity 91.5%;
Matches 526; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wordperfect
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CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Li
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US-09-053-453-2
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           Method For Identifying Or Isolating A Molecule And Molecules Identified Thereby
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                                                                                                                                                                   STATE: New York
ZIP: 10022
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 496.6; DB 3;
Pred. No. 1.5e-157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                    COMPUTER: IEM
COMPUTER: IEM
COMPUTER: IEM
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,980A
FILING DATE: 03-JANUARY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 6025191man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5410.1
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 931 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 931 base pairs
nucleic acid
EDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.2%;
Best Local Similarity 91.5%;
Matches 526; Conservative (
                                                                                                     ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: do TOPOLOGY: linear
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339 GGGAATGATTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACT 398
                                                361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
                                                         481 AAACAIGCCIGGACCCACAGACIGCGIGAGAGAAAAGCAGCIGGIGTIITAIGAAGAGGIC 540
                                                                                                                579 GAACATGCCTGGACCCACGACTGCGTGAGAAAACAGCTGGTGATTTATGAAGAGATC 638
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Pp 95
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Search completed: March 31, 2004, 17:26:48 Job time : 99 secs

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March 31, 2004, 16:39:19 ; Search time 389 Seconds (without alignments) 5512.734 Million cell updates/sec
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576
1 ATGAACGGAGACGCCTT.....ATGACGAGTAACTCCCCTCG 576
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| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUZ_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2458946 segs, 1861504846 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	i.		Seguence 5, Appin	Semience 5, Applia	Sequence 539, App	_	, ,	Sequence 8, Appil	, ,	, 6	Segrence 1000, Ap	Seducine 1392, Ap	Sequence 402, App	Sequence 7, Appli	sednence 6, Appli	Sequence 6, Appli
SUMMARIES ID	TTG _ 00 = 07E _ 0E G _ 3	T=989-676-60-50	US-10-177-277-5	US-10-117-937-599	US-09-849-602-13	US-10-207-655-84	US-10-117-937-6	US-09-833-039-2	US-10-177-277-2	US-09-954-531-1000	US-09-954-531-1392	TIS-10-150-150-200	TIS - 09 - 075 - 055 - 102	7 000 000 001	9-600-60-60-60	US-10-177-277-6
DB	-	10	14	15	10	14	15	10	14		9) (9 6	1	14
% Query Match Length	576	576	576	576	166	766	766	931	931	1309	1309	1249	576	7.70		576
% Query Match	100.0	100.0	100.0	100.0	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.1	83.7	83.7		83.7
Score	576	576	576	576	496.6	496.6	496.6	496.6	496.6	496.6	496.6	496	482.2	482.2	000	7.794
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US-09-833-039-1	TIS-10-177-27-1	(12 /17	-027-632-24	7000	07-986-70-7	1-029-386-2395	-10-027-632-33	3-027-632-330	US-10-027-632-148783	5 US-10-027-632-174961	US-10-027-632-1145	US-10-027-632-11451	US-10-027-632-32243	US-10-027-632-3224	US-09-814-353-18480	US-09-908-975-6728	US-09-981-353-84	K 20 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0		-747-OT	-10-133-013-26	-10-027-632-	-10-085-783A-1896	-10-242-5	-10-029-386-	-2178	-260A-1	41-181	9-909-87	92-	-632-	
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ALIGNMENTS

RESULT 1
Sequence 1, Application US/09978856
Sequence 1, Application US/09978856
Fublication No. US20030023057A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILD WITH A Sequence 1, Fanily Michael, Old,
Lloyd 1, Chen, Yao-Tseng
TILLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX
Members And Uses Thereof
CORRESPONDENCE 3.14
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Indibight & Jaworski L.L.P.
GITTY: New York City
STATE: New York City
STATE: Diskette, 3.5 inch, 144 kb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IDM
OPERATION SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION NUMBER: 09/796,780
FILING DATE: 110-Oct-2001
CLASSIFICATION NUMBER: 30,946
FILING DATE: 110-Oct-2001
ATTORNEY/ARRATION: CHARMONN:
APPLICATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
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REGISTRATION NUMBER: 30,946
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APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Furndschuh, Michael
TITLE OF INVENTION: Throw Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR PILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
                                                                                                                    Length 576;
                                                                                                                                             Indels
                                                                                                                Score 576; DB 10;
Pred. No. 2.8e-174;
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                                                                                                                                          0; Mismatches
                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
INCE CHARACTERISTICS:
LENGTH: 576 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
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// Publication No. US20030175960Al
// GENERAL INFORMATION:
                                                                                                              100.0%;
                                                       TOPOLOGY: linear
                                                                                                                          Local Similarity 100.
les 576; Conservative
  SEQUENCE
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US-09-833-039-5
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Sequence 5, Application US/10177277

Publication No. US20030185844A1

GENERAL INFORMATION:

APPLICANT: Sahin, Ugur

APPLICANT: Sahin, Ugur

APPLICANT: Steundschuh, Michael

APPLICANT: Stevanovic, Stefan

ITLLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determ:

ITLLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene

ITLLE OF INVENTION: Gene, and Uses Thereof

ITLLE OF INVENTION: Gene, and Uses Thereof

FILE REFERRNCE: LUD 5556.1

CURRENT PAPLICATION NUMBER: US/10/177, 277

CURRENT FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: US/09/344,040

PRIOR APPLICATION NUMBER: US 09/105,839

PRIOR FILING DATE: 1998-06-26

PRIOR FILING DATE: 1998-06-26
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                                                                                                                                                                                             0;
                                                                                                                                                    576;
                                                                                                                                                    Length
                                                                                                                                                                                             Indels
                                                                                                                                             Score 576; DB 10;
Pred. No. 2.8e-174;
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                                                                                                                                    Query Match
100.0%; Score 576; D
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 576; Conservative 0; Mismatches
                                           ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-833-039-5
SEQ ID NO 5
LENGTH: 576
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US-10-177-277-5
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                                                                                                                                                                    Length 576;
                                                                                                                                                                                                      Indels
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100.0%; Score 576; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-174;
Matches 576; Conservative 0; Mismatches 0;
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APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFRENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
               ; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 599
; LENGTH: 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09849602; Publication No. US20030165834A1; GENERAL INFORMATION:
                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
US-10-117-937-599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
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LENGTH: 766
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                                                                                                                                                        Length 576;
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                                                                                                                                               100.0%; Score 576; DB 14;
100.0%; Pred. No. 2.8e-174;
tive 0; Mismatches 0;
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APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-07-06
PRIOR PLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2001-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 599, Application US/10117937; Publication No. US20030220239A1
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 5
LENGTH: 576
                                                                                                                                                                                       Conservative
                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                               Query Match
Best Local Similarity
Matches 576; Conserv
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US-10-117-937-599
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91.5%; Pred. No. 1e-148;
ive 0; Mismatches 49; Indels
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US-10-117-937-6

Sequence 6, Application US/10117937

Publication No. US20030220239A1

GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAFIES CORP.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04

PRIOR FILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: US 60/337,017
FRIOR FILING DATE: 2001-11-07
FRIOR FILING DATE: 2001-04-06
FRIOR APPLICATION NUMBER: US 60/337,017
FRIOR FILING DATE: 2001-04-06
FRIOR FILING DATE: 2001-01-07

NUMBER OF SEQ ID NOS: 602

SEQ ID NO 6

LENGTHARE: FASTESQ for Mindows Version 4.0

SEQ ID NO 6
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US-10-117-937-6
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Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069,401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE PATENTIN VERSION 3.0
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Pred. No. 1e-148;
0; Mismatches 49; Indels 0;
                                                   Indels
          DB 10;
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                              1e-148;
        Score 496.6; I
Pred. No. 1e-14
0; Mismatches
        tch
al Similarity 91.5%;
526; Conservative
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Best Local Similarity 91.5%;
Matches 526; Conservative
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ORGANISM: Homo sapiens
    Query Match
Best Local Similarity
Matches 526; Conserv
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US-10-207-655-84
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APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Sterendschuh, Michael
APPLICANT: Freundschuh, Michael
APPLICANT: Sterendschuh, Michael
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determi
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
TITLE OF INVENTION: Gene, And Uses Thereof
TITLE OF INVENTION: Gene, And Uses Thereof
TITLE OF INVENTION WIMBER: US/10/177,277
CURRENT FILING DATE: 2002-06-21
FRIOR FILING DATE: 1999-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
      ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAGAGAGGGGAAAAGATG 218
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0; Mismatches 49;
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; Publication No. US20030185844A1
; GENERAL INFORMATION:
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| APPLICANT: Tureci, Ozlem
| APPLICANT: Sahin, Ugur
| APPLICANT: Sahin, Ugur
| APPLICANT: Sahin, Ugur
| APPLICANT: Pfreeundschuh, Michael
| APPLICANT: Pfreeundschuh, Michael
| TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
| FILE REFERENCE: LUD 562.1
| CURRENT APPLICATION NUMBER: US/09/833,039
| CURRENT FILING DATE: 1099-09-30
| PRIOR PILING DATE: 1999-06-25
| PRIOR FILING DATE: 1999-06-25
| PRIOR FILING DATE: 1998-06-26
| PRIOR FILING DATE: 1998-06-26
| PRIOR APPLICATION NUMBER: US 09/105,839
| PRIOR APPLICATION NUMBER: US 08/851,130
| PRIOR FILING DATE: 1997-05-05
| PRIOR FILING DATE: 1997-05-05
| NUMBER OF SEQ ID NOS: 129
| SEQ ID NO 2
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Pred. No. 1.1e-148;
0; Mismatches 49;
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JUNEAGL INTOCAMENT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Car
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Car
TITLE OF INVENTION: Gene Sets
FILE REPERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/60/234, 531
CURRENT APPLICATION NUMBER: US/60/234, 009
FRIOR APPLICATION NUMBER: US/60/234, 009
FRIOR FILING DATE: 2000-09-10
FRIOR FILING DATE: 2000-09-20
FRIOR APPLICATION NUMBER: US/60/234, 509
FRIOR APPLICATION NUMBER: US/60/234, 509
FRIOR APPLICATION NUMBER: US/60/234, 567
FRIOR PRILING DATE: 2000-09-22
FRIOR PRILING DATE: 2000-09-22
FRIOR PRILING DATE: 2000-09-22
FRIOR FILING DATE: 2000-09-22
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Patent No. US20020165180A1
GENERAL INFORMATION:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1309)
OTHER INFORMATION: n=a,t,g or
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Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
FILE REFERENCE: 689290-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                         ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAAGGAAGAAGAAGATG
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   TTACGAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAAGAAAAGAGAAAAAGATG
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Pred. No. 1.4e-148;
0; Mismatches 49;
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CURRENT PEPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/23,133
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFFWARE: PATENTIN VETSION 3.0
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Best Local Similarity 91.5%;
Matches 526; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1)...(1309)
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US-09-954-531-1000
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Sequence 2, Application US/09975856
Publication No. US20030023057A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gure, Ali O.; Tureci, Ozlem; Sahin, Ugur; Tsang, Solam;
Scanlan, Matthew J.; Knuth Alexander; Pfreundschuh, Michael; Old,
Lloyd J.; Chen, Yao-Tseng
IITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding SSX
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FILING DATE: 11-Oct-2001
CLASSIFICATION: CDASSIFICATION: CDASSIFICATION DATE: 09/796,780
PILING DATE: 2001-03-01
   0; Mismatches
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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STATE: New York
ZIP: 10103
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
         526; Conservative
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US-09-975-856-2
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Publication No. US20040009154A1
GENERAL INFORMATION:
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Markus
APPLICANT: Ringner, Paul
TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS;
FILE REPERRANCE: 11613.560VS11
CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
PRIOR FILING DATE: 2002-04-25
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                                                                                                                           Indels
                                                               Score 496.6; DB 9;
Pred. No. 1.4e-148;
0; Mismatches 49;
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Pred. No. 2.1e-148;
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91.3%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 402
LENGTH: 1249
                                                                  Query Match
Best Local Similarity 91.5%;
Matches 526; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
            US-09-954-531-1392
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US-10-159-563-402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 482.2; DB 10,
Pred. No. 3.7e-144;
0; Mismatches 58;
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APPLICANT: Sahin, Ugur
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
                     NAME: Hanson, No. US2003023057Alm
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5480
                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDENDESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          LENGTH: 576 nucleotides
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 89.9
Matches 517; Conservative
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US-09-833-039-6
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APPLICANT: Tureci, Ozlem
APPLICANT: Tureci, Uzur
APPLICANT: Sahin, Ugur
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determ:
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
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Pred. No. 3.7e-144;
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PRIOR APPLICATION NUMBER: US US/#US/#US/#ING PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 6
LENGTH: 576
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Publication No. US20030185844A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         83.7%;
89.9%;
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Best Local Similarity 89.9
Matches 517; Conservative
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Pred. No. 3.7e-144;
0; Mismatches 58; Indels 0;
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FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/10/177,277
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US/9/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
NUMBER OF SQ ID NOS: 132
SEQ ID NO 6
SEQ ID NO 6: 100 6
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Best Local Similarity 89.9%;
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March 31, 2004, 13:39:56; Search time 14 Seconds (without alignments) 4284.630 Million cell updates/sec
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1025
1 ATGAACGGAGGACGCCTT......ATGACGAGTAACTCCCCTCG 576
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                  - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          141681 segs, 52070155 residues
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Command line parameters:
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NOMN=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=200000000
-USR=US09975856_@CGM_1 1.16_@runat_31032004_132903_41378 -NCPI=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	O60224 homo sapien	homod	рошо		homo	P51815 homo sapien	homod	homod	070173 rattus norv	_	O54916 mus musculu		Q96d71 homo sapien		P17036 homo sapien	O62396 mus musculu	-	
SUMMARIES		QI	SSX4 HUMAN	SSX3_HUMAN	SSX2_HUMAN	SSX1_HUMAN	SSX5_HUMAN	ZN75_HUMAN	Z398_HUMAN	Z317 HUMAN	PK3G RAT	FMO1 CANFA	REP1 MOUSE	FMO1 PIG	REP1 HUMAN	SX11_CHICK	ZN38 HUMAN	ZF92 MOUSE	TC17 MOUSE	WR61_ARATH
		DB	Н		ч	ч	Н	Н	ч	Н	Н	П	Н	Н	Н	Н	Н	٦	Н	гН
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	% Query	Match	0.86	78.1	77.9	76.5	76.1	11.1	6.6	9.2	8.9	8.8	9.8	8.7	8.5	8.4	8.4	8.4	8.4	8.4
		Score	1004	801	798	784	780	113.5	101	94	89.5	88.5	88	87.5	87	86.5	86.5	86.5	86.5	98
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Q14511 homo sapien C9hcz1 homo sapien P5153 homo sapien C58851 methanococc O9nqx6 homo sapien P17636 oryctolagus Q96jc4 homo sapien Q61967 mus musculu Q9h2D0 homo sapien P04932 plasmodium P04932 plasmodium Q16587 homo sapien Q16587 homo sapien P95201 homo sapien P1827 glycine max	P38904 saccharomyc P75080 mycoplasma P17023 homo sapien Q943m9 homo sapien Q84byb7 canis famil P21506 homo sapien Q96673 homo sapien P78347 h general t Q01740 homo sapien Q9bx82 homo sapien	IS 8 AA. ate) odate) Vertebrata; Ruteleostomi; i; Hominidae; Homo.	Scanlan M.J., Jager E., T., rs transcribed in normal	se L.H., Derge J.G., L., Shenmen C.M., Schuler G.D., M., Schaefer C.F., Bhat N.K., A., Rubin G.M., Hong L., F., Casavant T.L., Scheetz T.E., G., Abramson R.D., Mullahy S.U., Malek J.A., Gunaratne P.H., Malek J.A., Gunaratne P.H., M., Abramson R.D., Mullahy S.W., M., Abramson R.D., Mullahy S.W., M., Abramson R.D., Mullahy S.W., M., Myers R.M., Skalska U., Smailus D.E., Marra M.A., Skalska U., Smailus D.E.,
834 1 CASE 834 1 CASE 680 1 Z334 429 1 EINSK, 429 1 Z331 524 1 Z331 102 1 ADD 102 1 ADD 103 1 MSP1 1639 1 ZN74, 645 1 ZN74, 649 1 ZN74, 649 1 ZN74, 639 1 GLCS	0 0 14395 1 14443 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ALIGNMEN. ARD; PRT; 18 Created) Last sequence upd Last annotation up	.A. 2; PubMed=9378559; eci O., Sahin U., Tsang S., Scendschuh M., Old L.J., Chen YT ne family with several members n cancer."; 72:965-971(1997).	SEQUENCE FROM N.A. TISGUENCE FROM N.A. TISGUES TO bubMed=12477932; MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Hopkins R.F., Jordan H., Moore T., Max S.I., Walling G.N., Hopkins R.F., Jordan H., Moore T., Max S.I., Walbing J., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gub Fishey J., Helton E., Ketteman M., Madan A., Rodrigues Whiting M., Madan A., Young A.C., Shales S., Worley K.C., Stales S., Worley K., Stales S., Whyers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smail Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
0 222 22 22 22 22 22 22 22 22 22 22 22 2	81.5 81.5 81.5 81.7 80.5 77 80.5 77 79.5 77	HUMAN SSX4 HUMAN C60224 C90UU9; 15-UUL-1999 (Re 15-UUL-1999 (Re 110-OCT-2003 (Re SSX4 protein. SSX4. HOMO Sapiens (H BUMATYOCH; META	RN [1] RX MEDLINE=98021352; PubMe RA Gure A.O., Tuereci O., RA Knuth A., Fteundschuh RT "SSX: a multigene famili RT testis and human cancer RL Int. J. Cancer 72:965-9	RC TISGUENCE FROM N. RZ TISGUENCE FROM N. RAALSCHUL S.F., ZRAALSCHUL Z.F., ZRAALSCHUL Z.F., ZRAALSCHUL Z.F., ZRAALSCHULZ

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161 İystishlarıpThrHisArgLeuArgGluArgLysGluLeuValValTyrGluGluIle 180
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Gure A.O., Tuereci O., Sahin U., Tsang S., Scanlan M.J., Jager E.,

Knuth A., Pfreundschuh M., Old L.J., Chen Y.-T.;

"SX: a multigene family with several members transcribed in normal

testis and human cancer.";

Int. J. Cancer 72:965-971(1997).

-!- FUNCTION: Could act as a modulator of transcription.
-!- FUNCTION: Could act to the SSX family.
-!- SIMILARITY: Belongs to the SSX family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  de Leeuw B., Balemans M., Geurts van Kessel A.; "A novel Kruppel-associated box containing the SSX gene (SSX3) on human X chromosome is not implicated in t(X;18)-positive synovial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genew, HONC:11337; SSX3.

MIN, 300325; -.

InterPro; IPR001909; KRAB.

InterPro; IPR003655; KRAB_related.

Rea, PF03152; KRAB; 1.

SWART; SM00349; KRAB; 1.

ROSSITE; PS50806; KRAB_RELATED; 1.

ROSITE; PS50806; KRAB_RELATED; 1.

ROMILIGENE family; Transcription regulation.

CONFLICT 95 95 L -> Q (IN REF. 2).

SEQUENCE 188 AA; 21682 MW; 368C7487C1450E72 CRC64;
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Mismatches:
Indels:
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                   541 AGCGACCCTGAGGAAGATGACGAG 564
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Query Match:
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ID SSX3_HUMAN
ID SSX3_HUMAN
AC 099303_H
DT 15-DEC;
DE SSX3_P
GN SSX3_P
GN Mammal;
GN MEDLINE
RR MEDLINE
GN MED
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                                                                                                               SEQUENCE OF 1-155 FROM N.A.
Blechschwidt K., Nyakatura G., Strom T.M., Drescher B., Menzel U., Meindl A., Rosenthal A., Sosenthal A., Sosenthal A., Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Could act as a modulator of transcription.
-!- SIMILARITY: Belongs to the SSX family.
-!- SIMILARITY: Contains 1 KRAB-related domain.
   Generation and initial analysis of more than 15,000 full-length
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InterPro; IPR003655; KRAB_related.
InterPro; IPR003655; KRAB_related.
Pfam; PF01352; KRAB; 1.
PR051TE; PS0806; KRAB; 1.
PR051TE; PS0806; KRAB_RELATED; 1.
Multigene family; Transcription regulation.
DOWAIN
20 83 KRAB_RELATED.
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                              human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Indels:
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Matches:
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MEDLINE=9529374; PubMed=7539744;
Crew A.J., Clark J., Fisher C., Gill S., Grimer R., Chand A.,
Crew A.J., Clark J., Cooper C.S.;
Shipley J., Gusterson B.A., Cooper C.S.;
Flusion of SYT to two genes, SSX1 and SSX2, encoding proteins with
"Fusion of SYT to two genes, SSX1 and synovial sarcoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology to the Kruppel-associated box in human synovial sarcoma.";
EMBO J. 14:2333-2340(1995).
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSX2 HUMAN STANDARD; PRT; 188 AA.
016385; 016404; Q961P7;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
SSX2 protein (Synovial sarcoma, X breakpoint 2) (SSX) (HOM-MEL-40)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Gaps:
                                  US-09-975-856-1 (1-576) x SSX3_HUMAN (1-188)
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A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Britchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong I., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., A Brownstein M.J., Usdin T.B., Toohlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McZwan P.J., McKennan K.J., Malek J.A., Gunaratne P.H., A Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahabay J., Helton E., Ketteman M., Madan A.W., Rodriques S., Sanchez A., Mhiring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Homera A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Helpth M. Malaysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=95338816; PubMed=7951320; Clark J., Rocques P.J., Crew A.J., Gill S., Shipley J., Chan A.M.-L., Gusterson B.A., Cooper C.S.; "Identification of novel genes, SYT and SSX, involved in the t(X,18) [pll.2;qll.2) translocation found in human synovial sarcoma."; Nat. Genet. 7:502-508(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Leeuw B., Balemans M., Olde Weghuis D., Geurts van Kessel A.; "Identification of two alternative fusion genes, SYT-SSXI and SYT-SSXZ, in t(X,18)(pll.2;qll.2)-positive synovial sarcomas."; Hum. Mol. Genet. 4:1099(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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MEDLINE=96094743; PubMed=7495284;
Fligman I., Lonardo F., Jhanwar S.C., Gerald W.L., Woodruff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 111-188 FROM N.A. (SSXT-SSX2 FUSION PROTEIN) TISSUE=Synovial sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; S79332; AAB35379.1; -.
EMBL; X79200; -; NOT ANNOTATED CDS.
EMBL; S79894; AAB3574.1; ALT_INIT.
PIR; S55058; S55058.
Genew; HGNC:11336; SSX2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Synovial sarcoma;
MEDLINE=95384157; Pubmed=7655467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences.
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121 AAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGAAGAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                      MetAsnGlyAspAspAlaPheAlaArgArgProThrValGlyAlaGlnileProGluLys
                                                                                                                                           BREAKPOINT FOR TRANSLOCATION TO FORM THE SXT-SX2Z PUSION PROTEIN (RARE).
BREAKPOINT FOR ITANSLOCATION TO FORM THE SXXT-SXXZ FUSION PROTEIN.
             GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS
                         InterPro; IPR01909; KRAB.
InterPro; IPR03855; KRAB.
Fram, PF01352; KRAB, 1.
PR038TT; SM00349; KRAB, 1.
PROSITE; PSS0806; KRAB_RELATED; 1.
Chromosomal translocation; Proto-oncogene; Multigene family;
                                                                                                                                                                                                     R -> P (IN REF. 2; AAH07343).
BF5D18AA5F45B1B1 CRC64;
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Matches:
                                                                                                                                  KRAB-RELATED,
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DOMAIN 20 83
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188 AA;
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                                                                                                                                                                                                                                                                                                      Local Similarity:
                                                                                                                                              89
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15-DEC-1998
15-DEC-1998
 MIM; 300192;
                                                                                                                                                                                                                                              Alignment Scores:
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ID SSX1_HU
AC Q16384;
DT 15-DEC-
DT 15-DEC-
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(Rel. 37, Created) (Rel. 37, Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A MEDILNE=22388257; PubMed=12477932;

RA MEDILNE=22388257; PubMed=12477932;

RA Klauner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altachul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K.,

RA Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hgieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hgieh F.,

RA Datchenkov L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muuxny D.W., Sodergram B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Gremuz J., Myers R.M.,

RA Sodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

Ra Generation and initial analysis of more than 15,000 full-length

RI human and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJIRE=95.84157; PubMed=7655467;

MEDIJIRE=95.84157; PubMed=7655467;

de Leeuw B., Balemans M., Olde Neghuis D., Geurts van Kessel A.;

Infentification of two alternative fusion genes, SYT-SSXI and

"Identification of two alternative fusion genes, SYT-SSXI and

"Identification of two alternative fusion genes, SYT-SSXI and

"IDENTIFICATION: Could act as a modulator of transcription.

-! FUNCTION: Could act as a modulator of transcription.

-! FUNCTION: Could act as a modulator of transcription.

-! FUNCTION: Could act as a modulator of transcription.

-! FUNCTION: Could act as a modulator of transcription.

-! FUNCTION: Could act as a modulator of transcription.

-! FUNCTION: Could act as a modulator of the synovial sercoma and epithelial cell lines.

-! DISEASE: Participates in a t(X;18) (p11.2;q11.2) chromosomal translocation that is specifically found in more than 80% of synovial sercoma and produces the SSXT-SSXI or SSXT-SSXI for SXT-SSXI or SSXT-SSXI or transforming activity. Heterogeneity in the position of the breakpoint can occur (low freequency).

-! SIMILARITY: Belongs to the SSX family.

-! SIMILARITY: Belongs to the SSX family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colon,
                                                                                                                                                                                                                                            MEDINE-95292974, PubMed=7539744; Crew A.J., Clark J., Fisher C., Gill S., Grimer R., Chand A., Shipley J., Gusterson B.A., Cooper C.S.; Fusion of SYT to two genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel-associated box in human synovial sarcoma."; EMBO J. 14:2333-2340(1995).
                                                                                                          Euteleostomi;
                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
  nast annotation update)
sarcoma, X breakpoint 1)
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     Last
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                     SSX1 protein (Synovial
  42
                                                                         (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=9606;
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                                                                            sapiens
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CTAGGTTTCAAGGTCACCTCCCACCTTTCATGCGTAAAACGGGCTGCAGACTTCCAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGAACGGAGACGACGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAAG
                                                                                                                                                                                                   BREAKPOINT FOR TRANSLOCATION TO FORM THE
                                                                                                                                                                                                             SSXT-SSXI FUSION PROTEIN (RARE).
BREAKPOINT FOR TRANSLOCATION TO FORM THE
SXXT-SSXI FUSION PROTEIN.
E440D1B2AE3AE9F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 CCCCCGGGAAATCCAAGTACCTTGGAGAATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                                                         PROSITE; PS50806; KRAB RELATED; 1.
Chromosomal translocation; Proto-oncogene; Multigene family;
        PIR; S55057; S55057.

Genew; HGNC:11335; SSX1.

MIN; 312820; -.

GO; GO:0005634; C:nucleus; TAS.

GO; GO:0005714; F:transcription co-repressor activity; TAS.

InterPro; IPR001309; KRAB.

InterPro; IPR001309; KRAB.

Ffam; PF01352; KRAB; 1.

SMART; SM0349; KRAB; 1.
                                                                                                                                                                                                                                                                                                   188
1188
9 4 0
0 0
                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                        21931 MW;
                                                                                                                                                                                                                                                                                           8.96e-70
784.00
84.04%
79.26%
 AAB35378.1;
                                                                                                                                                                     Transcription regulation.

DOMAIN 20 83
SITE 62 63
                                                                                                                                                                                                                             111
                                                                                                                                                                                                                                                        188 AA;
                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                            110
 879325;
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SSX5_HUMAN
ID SSX5_HUMAN
                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
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188 AA

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STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Strausberg R.D., Feingold E.A., Grouse D.H., Derge J.G.,
Alachine F.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
As Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
Antiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
Antiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2022).

L. FUNCTION: Could act as a modulator of transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 300327; -.
InterPro; IPR003655; KRAB.
InterPro; IPR003655; KRAB_related.
Féan; PF01352; KRAB; 1.
SMART; SM00349; KRAB; 1.
SMART; SM00349; KRAB; 1.
Multigene family; Transcription regulation; Alternative splicing.
DOMAIN 23 KABA-RELATED.
23 K -> KHPWRQVCDRGIHLVNLSPFWKVGREPASSIKALLC
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gure A.O., Tuereci O., Sahin U., Tsang S., Scanlan M.J., Jager E., Knuth A., Pfreundschuh M., Old L.J., Chen Y.-T., "SSX: a multigene family with several members transcribed in normal testis and human cancer.";
                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note=No experimental confirmation available, -!- SIMILARITY: Belongs to the SSX family. -!- SIMILARITY: Contains 1 KRAB-related domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=060225-2; Sequence=VSP_006274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=060225-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Skin;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98021352; PubMed=9378559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Int. J. Cancer 72:965-971(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U90842; AAC05821.1; -. EMBL; BC016640; AAH16640.1;
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MIM; 300327; -.
O60225; Q96AW3;
15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                      SSX5 protein.
SSX5.
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200
228
228
256
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Pred. No.:
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SEQUENCE
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                                                                                                                                                                                                                        181 CTAGGTITCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGACTTCCAC 240
                                                                                                                                                                                                                                                         GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
                                                                                                                                                                                                                                                                      81 GlyAsnAspPheAspAsnAspProAsnArgGlyAsnGlnValGluHisProGlnMetThr 100
                                                                                                                                                                                                                                                                                         TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGGAAA 360
                                                                                                                                                                                                                                                                                                   AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC 420
                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                   1 MetasnGlyAspAspAspAlaPheValArgArgProArgValGlySerGlnIleProGlnLys 20
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                                                                                                                                                                                                                                                                                                                                                         CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                        481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] —
SEQUENCE FROM N.A.
IISSUE-Lung fibroblast;
MEDLINE-94116987; PubMed=8288223;
Willa A., Zucchi I., Pilia G., Strina D., Susani L., Morali F.,
GRGEAR (in isoform 2).
/FTId=VSP 006274.
P -> Q (IN REF. 2).
AD2A3096931C5E37 CRC64;
                                                 1188
144
100
000
                                                Length:
Matches:
Conservative:
                                                                        Mismatches:
Indels:
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zhor finger protein 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 AA
                                                                                          Gaps:
                                                                                                         x SSX5 HUMAN (1-188)
                                                                                                                                                                                                                                                                                                                                                                                                                         541 AGCGACCCTGAGGAAGATGACGAG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAspProProGluAspAspGlu 188
                       21628 MW;
                                         2.23e-69
780.00
85.11%
77.66%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
               184 1
188 AA;
                                                                                                        US-09-975-856-1 (1-576)
                                                                        Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                Percent Similarity:
                                       Alignment Scores:
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P51815;
                CONFLICT
                                                                                                                                                          61
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GO; GO:0008270; F: Tainc ion binding; NAS.

GO; GO:0008270; F: Tainc ion binding; NAS.

RO; GO:0008270; F: Tainc ion binding; NAS.

GO; GO:0008270; F: Tainc ion binding; NAS.

RO; GO:0008270; F: Tainc ion binding; NAS.

RO; GO:0008270; F: Tainc ion binding; NAS.

RO; GO:0008270; F: Tainc ion binding; CALL.

RO; GO:0008270; F: Tainc ion binding; CALL.

RO; GO:0008270; F: Tainc ion; CALL.

RO; GO:0008270; F: Tainc ion; CALL.

RO; GO:0008270; F: Tainc ion; CALL.

RO; FROSITE; PSSO0187; F: Tainc ion; DNA-binding; Zinc-finger; Metal-binding;

Muchast mortain.
                                                                                                                                             [2] SEQUENCE OF 139-289 FROM N.A. BAZE N., ROSATÍ M., ROCCHÍ M., Marino M., Archidiacono N., Franze N., Rosatí M., Rocchí M., Ballabio A., Grimaldí G., Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: May be involved in transcriptional regulation.
-! STUBCELLULAR LOCATION: Nuclear (Potential).
-! SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
Patrosso C., Frattini A., Lucchini F., Repetto M., Sacco M.G., Zoppe M., Vezzoni P., "ZNF75: isolation of a cDNA clone of the KRAB zinc finger gene subfamily mapped in YACs 1 Mb telomeric of HBRT."; Genomics 18:223-229(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2H2-TYPE 1.
C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
C2H2-TYPE 5.
V; 96E7B00BF1DF64DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289
37
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39
43
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-!- SIMILARITY: Contains 5 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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Indels:
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42.25%
26.06%
11.07%
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Genew; HGNC:13145; ZNF75.
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DOMAIN 14 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 KRAB domain.
-!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
gene model prediction.
                                              SECUENCE OF 234-642 FROM N.A.

MEDLINE=20181126; PubMed=10718199;

MEDLINE=20181126; PubMed=10718199;

Magage T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. XVI

The complete sequences of 150 new cDNA clones from brain which code

for large proteins in vitro.";

DNA Res. 7:65-73(2000).

-!- FUNCTION: Function as a transcriptional activator.

-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:18373; ZNF398.

George Go: Go:0005634; C:nucleus; NAS.

GO: GO:0016563; F:transcriptional activator activity; NAS.

GO: GO:0006355; F:transcription of transcription, DNA-dependent; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold=Q@TD17-2; Sequence=VSP 006926;
INDUCTION: By estrogen receptor alpha.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMAKI; SMUNDSS), MINIONES, TRAB; 1, PROSITE; PSSO005; KRAB; 1, PROSITE; PSSO0028; ZINC FINGER C2H2 1; 7. PROSITE; PSSO157; ZINC FINGER C2H2 2; 8. Transcription regulation; Activator; DNA-binding; Zinc-finger; Metal-binding; Nuclear protein; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69AA38FCD84FF633 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=p71;
IsoId=Q8TD17-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2H2-TYPE (ATYPICAL)
C2H2-TYPE (DEGENERAT
C2H2-TYPE.
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Matches:
Conservative:
Mismatches:
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C2H2-TYPE.
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC004890; AAD45824.1; ALT_SEQ.
EMBL; BC043295; AAH43295.1; -.
EMBL; AB037760; BAA92577.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001909; KRAB.
InterPro; IPR001909; KRAB.
Fram: PF01352; KRAB; 1.
Pfam; PF01352; KRAB; 1.
Pfam; PF00096; zf-C2H2; 8.
ProDom; PD000003; znf_C2H2; 2.
SWART; SM00149; KRAB; 1.
SWART; SM00149; KRAB; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY049744; AAK92789.1; -. EMBL; AY049743; AAK92788.1; -.
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41.60%
24.80%
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Best Local Similarity:
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180 IleSerMetAspTyrAlaileAsnGlnProAspValLeuSerGlnIleGlnProGluGly 199
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                                                                                                                    LysValProValAlaPheAspAspValSerIleTyrPheSerThrProGluTrpGluLys 159
                                                                                                                                                      118 ATGAAATCCTCGGAGAAAATCGTCTATGTG---TATATGAAGCTAAACTATGAGGTCATG 174
                                                                                                                                                                                                                       175 ACTAAACTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGAC 234
                                                                                                                                                                                                                                                                                                                                                             ATGACTTTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koike T., Sawada Ki K.;
"Molecular cloning and characterization of a KRAB-containing zinc
finger protein, ZNE317, and its 88:771-779 (2001).
-!- FUNCTION: May function as a transcription factor. May play an
important role in erythroid maturation and lymphoid proliferation.
-!- SUBCELLUIAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                         TTCCACGGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAG
                                                                                  AAGTTACGAAAGGCCTTCGATGATATTGCCCAAATACTTCTCTAAGAAAAGAGTGGGAAAAG
                                                                                                                                                                                                                                                                                                                      200 GluHisAsnThrGlu-----AspGlnAlaGlyProGluGluSerGlu-----
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IsoId=Q96PQ6-4; Sequence=VSP 006915;
TISSUE SPECIFICITY: Isoforms I and 3 are ubiquitously expressed.
Isoforms 3 and 4 are expressed only in lymphocytes, spleen, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMÍLARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZNF317.

ZNF317.

ZNF317.

From sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
MEDLINE=21547764; PubMed=11688974;
Takashima H., Nishio H., Wakao H., Nishio M., Koizumi K., Oda A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1; Synonyms=ZNF317-1;
IsoId=Q96PQ6-2; Sequence=VSP_006916;
Name=3; Synonyms=ZNF317-3;
IsoId=Q96PQ6-3; Sequence=VSP_006915; VSP_006916;
     32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=4;
Name=2; Synonyms=ZNF317-2;
IsoId=Q96PQ6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096PO6; 096PM0; 096PM1; 096PT2; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
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   Indels:
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240 GlnValGlyAlaPro 244
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGATGATATTGCCAAATACTTCTCTAAGAAAGAGTGGGAAAAGATGAAATCCTCGGAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AAAATCGTCTATGTGTATATGAAGCTA---AACTATGAGGTCATGACTAAACTAGGTTTC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 AAGGICACCTCCCACCTTTCAIG---CGIAGIAAACGGGCTGCAGACTICCACGGGAAI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ArglysLeuTyrLysAspValMetLeuGluAsnTyrSerAsnLeuThrSerLeuGlyTyr 98
                                                                                                                                                                                                               ### PF01352; KRAB; 1.

Pfam; PF01352; KRAB; 1.

Pfam; PF00096; zf-C2H2; 13.

SMART; SM00349; KRAB; 1.

SMART; SM00355; ZnR_C2H2; 13.

PROSITE; PS50805; KRAB; 1.

PROSITE; PS50805; ZINC_FINGER_C2H2_1; 13.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.

Transcription regulation; Zinc_finger; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform 3 and isoform 4)./FIId=VSP_006915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (in isoform 1 and P_006916.
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Matches:
Conservative:
Mismatches:
Indels:
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C2H2 - TYPB.
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C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                        KRAB
                                                                                                          EMBL; AF275255; AAL29188.1; --
EMBL; AF148135; AAL29182.1; --
EMBL; AF307095; AAL29190.1; --
EMBL; AF307097; AAL29191.1; --
PIR; JC7779; JC7779.
InterPro; IPR001909; KRAB.
InterPro; IPR001909; RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67941 MW;
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94.00
47.62%
30.48%
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ZN_FING
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247 GATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAAACGTCCTCAGATGACTTTTCGGC 306

8 8 8

119 GluArgGlyAlaHisGlnGlyAlaCysAlaAspTrpGluThrProSerLysThrLysTrp

307 AGCCTC-----CAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGGAGGAAGAA 360

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SMART; SM00146; PI3Kc; 1.
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                                                                                                                                                                                                                                                                          SEQUENCE
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         DAR DAR DAR DAR SOLUTION AND DAR MANAGEMENT OF STATE AND DARK MANAGEMENT O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE=Regenerating liver;

MEDLINE=98184888; PubMed=9516481;

MEDLINE=98184888; Submed=9516481;

Suzuki M., Matsuno S., Konto B.,

"A novel class II phosphoinositide 3-kinase predominantly expressed in the liver and its enhanced expression during liver regeneration.";

J. Blol. Chem. 273:7731-7736(1998).

-!- FUNCTION: IN VITRO, PHOSPHORYLATES PTDINS AND PTDINS4P BUT NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phosphatidylinositel 4-phosphate 3-kinase C2 domain-containing polypeptide (EC 2.7.1.154) (Phosphoinositide 3-Kinase-C2-gamma)
(PtdIns-3-kinase C2 gamma) (P13K-C2gamma).
                                                                                                                                                                                                      PRT; 1505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR008938; ARM.
InterPro; IPR000008; C2.
InterPro; IPR000009; C2.
InterPro; IPR000403; P13 P14 kinase.
InterPro; IPR002420; P13K_C2.
InterPro; IPR000341; P13K_ras_bind.
InterPro; IPR001263; P13Kas_bind.
InterPro; IPR001263; P13Kas_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00168; C2; 1.
Pfam, PF000454; Pi3 PI4 kinase; 1.
Pfam; PF00792; PI3K_C2; 1.
Pfam; PF00794; PI3K_Kbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB009636; BAA25634.1; -
                                                                      361 AATGGTTTGAAGGAA 375
                                                                                                             Aladiyieuglydiu 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00239; C2; 2.
SMART; SM00142; PI3K C2; 1.
SMART; SM00144; PI3K rbd; 1.
SMART; SM00145; PI3Ka; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00613; PI3Ka; 1.
Pfam; PF00787; PX; 1.
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00168;
                                                                                                                                                                                                      PK3G RAT
                                                                                                                                                                                                                                                                                                                                                                                     PIK3C2G
                                                                                                                                                          RESULT 9
PK3G_RAT
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490 AGGCATGTTTCCCCCCTTTTGGGTCCAGATGTCTTGTTAATCTTCTCCAAGGTACTTGGAT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 TTCCCGGGGGGCACAGCTGTTTCCCATCATTTTGTGGGCCAGATGCCTCTGGCACTTCCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 GlyGluAspProArgPheSerAlaLeuThrProSerSerThrGlyLeuAspLysCysHis 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 CAAAATCATTCCCGTGGAAGTCTGCAGCCCGTTTACTACGCATGAAAGGTGGGAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 TCAAACCATTTTCTTCCTCTGCTGCTTCTTGGGCATGATCTTCGGGAAGATTCTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 GGCTGCCGAAAGTCATCTGAGGACGTTCAACCTGATTCCTGTGGTTTCGATCGT---TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lattard V., Longin-Sauvageon C., Lachuer J., Buronfosse T., Benoit B. "Cloning, sequencing and tissue dependent expression of FMO1 and FMO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: This protein is involved in the oxidative metabolism of a variety of xenobiotics such as drugs and pesticides.
-!- CATALYTIC ACTIVITY: N, N-dimethylaniline + NADPH + O(2) = N, N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dimethylaniline monooxygenase [N-oxide forming] 1 (BC 1.14.13.8)
(Hepatic flavin-containing monooxygenase 1) (FMO 1) (Dimethylaniline oxidase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 CCTIGAAACCTAGTTTAGTCATGACCTCATAGTTTAGCTTCATATACA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 GinginglyGinSerglyThrGluHisCysAsnTyrTyrVal-----
                                                                                                                                                                                                                               1402 1499 C2 DOMAIN.
1505 AA; 170974 MW; 5ED4C2239968C4B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the dog."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     1505
33
16
50
17
5
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 AA
                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-975-856-1 (1-576) x PK3G RAT (1-1505)
                                                                                                                                                                                                                                                                                                                     0.95
89.50
42.24%
28.45%
8.89%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                            1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
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human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                target, RalBP1.
                                                                                                                                                                                                                                 rissum=Muscle;
                                                                protein 1).
      HERE TO THE TREE TO THE TOTAL THE TOTAL TO T
                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 ACTOGICATOTICCICAGGGICGCIGAICTOTICATAAACCACCAGCIGCITICICICAC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505 GCAGTCTGTGGGTCCAGGCATGTTTCCCCCTTTTGGGTCCAGATGTCTTGTTAATCTTCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 CCAAGGIACTIGGATTICCCGGGGGGCACAGCTGTTICCCATCATTITGTGGGCCAGATG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 CCICTGGCACTICCITCAAACCATITICTICCTCTGCTGGCTTCTTGGGCATGATCTTCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 GGAAGATTCTCTGGAGGCTGCCGAAAGTCATCTGAGGACGTTCAACCTGATTCCTGTGGT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ArgpheSerLeuLeuLysCysIl 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 TTCGATCGTTACCAAAATCATTCCCGTGGAAGTCTGCAGCCCGTTTACTACGCATGAAAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||| :::||||::::: ||||||| ||| ||| ProAsnTyrValProAsnSerGlnPheLeuGluTyrLeuLysMetTyrAla-Asn---- 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------PheProGluAspTyr 77
                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0419; ADXEDTASE.
PRINTS; PR00368; FADPNR.
PRINTS; PR00370; FMOXYGENASE.
Oxidoreductase; Monooxygenase; NADP; Flavoprotein; FAD; Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 ------ValSerAsnSerCysLysGluMetSerCys----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Multigene family; Acetylation.
INIT_MET 0 BY SIMILARITY.
MOD_RES 1 1 ACETYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADP (POTENTIAL).
9F3458484540521F CRC64;
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14
14
40
40
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Mismatches:
Indels:
dimethylaniline N-oxide + NADP(+) + H(2) O. COFACTOR: FAD (By similarity).
SUBCELLULAR LOCATION: Microsomal.
TISSUE SPECIFICITY: Liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 -----TyrSerAspPhePro------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                743 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAD (ADP PART)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                               SIMILARITY: Belongs to the FMO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-975-856-1 (1-576) x FMO1_CANFA (1-531)
                                                                                                                                                                                                                                                                                EMBL; AF384053; AAK97433.1; -.
InterPro; IPR00159; Adrndx_reductase.
InterPro; IPR001327; PAD_pyr_redox.
InterPro; IPR000960; Flav cont_mnoxgn.
Pfam; PF00743; FMO-like; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 FA
195 NA
59927 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _REP1 MOUSE STANDARD;
054916; Q8C9J9; Q99LR8;
10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.996
88.50
38.21%
26.83%
8.79%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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MOD RES
NP BIND
NP BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
REP1_MOUSE
ID REP1_MC
AC O54916;
DT 10-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
g
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10-COT-2003 (Rel. 44, Last suncertion update)
25 RAIBPI associated Eps domain containing protein I (RalBDI-interacting protein I) Co-COT-2003 (Rel. 44, Last suncertion update)
26 RAIBPI associated Eps domain containing protein I (RalBDI-interacting protein II (RalBDI-interacting protein)
27 RAIBPI associated Eps domain containing protein II (RalBDI-interacting protein)
28 RAIBPI associated Eps domain containing protein II (RalBDI-interacting marginello 1009)
28 RAIBPI ASSOCIATED (1000)
29 RAIBPI (1000)
20 RAIBPI (1000)
21 RAIBPI (1000)
21 RAIBPI (1000)
22 RAIBPI (1000)
23 RAIBPI (1000)
24 RAIBPI (1000)
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27 RAIBPI (1000)
28 RAIBPI (1000)
27 RAIBPI (1000)
28 RAIBPI (1000)
28 RAIBPI (1000)
28 RAIBPI (1000)
28 RAIBPI (1000)
29 RAIBPI (1000)
20 RAIBP
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                                                                                                                                                                                                                                                                                             available;
--- TISSUE SPECIFICITY: Expressed in all tissues examined. The highest level expression was found in the kidney and testis.
--- PIM: EGF stimulates phosphorylation on Tyr-residues.
--- SIMILARITY: Contains 1 EH domain.
--- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
--- CAUTION: Ref. 3 sequence differs from that shown due to a
                                                                                                                                                   GRB2. Binding to RALBP1 does not affect its Ral-binding activity. Forms a complex with the SH3 domains of CRK and GRB2 which may link it to am EGF-responsive tyrosine kinase.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00018; EF HAND; 1.
PROSITE; PS50031; EH; 1.
Calcium-binding; Coiled coil; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWETFSERSSSQTLTQFDSNIAPADPDTAIVHPV ->
VSKTSLSLLEISLFTGRSFKQDRFTAGYLQYAHTP (in
          -!- FUNCTION: May coordinate the cellular actions of activated EGF receptors and Ral-GTPases.
                                                                                                                                       SUBUNIT: Homodimer (Potential). Interacts with RALBP1, CRK and
                                                                                                                                                                                                                                                     Name=2;
IsoId=054916-2; Sequence=VSP_007956, VSP_007957;
Note=Due to intron retention. No experimental confirmation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL).
PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25510D11254CF4A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH RALBP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (in isoform 2).
/FIId=VSP_007957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743
25
25
41
61
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EF-HAND (POTENTIAL).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      007956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                          Name=1;
IsoId=O54916-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF031939; AAB94736.1; -.
EMBL; AK041967; BAC31117.1; ALT_INIT.
EMBL; BC002256; AAH02256.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; IFI6; 18-JUL-01.
MGD; MGI:1196373; Repsl.
InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_homology.
Pfam; PF00036; efhand; 1.
SMART; SM00027; EH; 1.
                                                                                                                                                                                                                                                                                                                                                                                              frameshift in position 719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80598 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.18
88.00
38.92%
23.95%
8.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; T09173; T09173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
279
488
692
692
368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE
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CA BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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Query Match: DB:

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TACTTCTCTAAGAAAGAGTGGGAAAAGATGAAATCCTCGGAGAAAATCGTCTATGTGTTAT 150
                                                                                                                                                                                                                                                                                                                              ----AGGAATCAGGTTGAACGTCCTCAGATGACTTTCGGCAGCCTCCAG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435
                                                                                                                                                                                                                                                           270
                                                                                                                                                                                                                                                                                                                                                                                                       316 AGAATCTTCCCGAAGATCATGCCCCAAGAAGCCAGCAGGAAGAAAATGGTTTGAAGGAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 HisThr-TrpArgLysHisSerArgHis-----ProSerGlyGlyAsnSerGluArgPr 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 -----GlubroAlaSerProValValSerProGlnGln---SerProProThrSerPro 123
                                                                      --Tyr 18
                                                                                                                                            19 IleAlaLeuLysLeuValAlaValAlaGlnSerGlyPheProLeuArgValGluSerIle 38
                                                                                                                                                                                                   39 AsnThrValLysAspLeuProLeuProArgPheValAlaSerLysAsnGluGlnGluSer 58
                                                                                                                                                                                                                                                                              79 ProProProGlyArgGlyGlnValLysLysGlyProGlySerHisAspAlaValGln 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 GTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGCCCCCCCGGGAAATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90343821; PubMed=2383273; Guan S.H., Falick A.M., Cashman J.R.; Murterminus determination: FAD and NADP binding domain mapping of hog liver flavin-containing monooxygenase by tandem mass spectrometry."; Biochem. Biophys. Res. Commun. 170:937-943(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dimethylaniline monooxygenase [N-oxide forming] 1 (EC 1.14.13.8)
(Hepatic flavin-containing monooxygenase 1) (FWO 1) (Dimethylaniline oxidase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The flavin-containing monooxygenase expressed in pig liver: primary sequence, distribution, and evidence for a single gene."; Biochemistry 29:119-124(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
MEDLINE=90212556; PubMed=2322534;
Gasser R., Tynes R.E., Lawton M.P., Korsmeyer K.K., Ziegler D.M.,
Philpot R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436 AGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGGAAACATG-
                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ProArgProSerAlaGluGlnGln-----
                                                                                                                                                                                                                                                     223 CGGGCTGCAGACTTCCACGGGAATGATTTTGGTAACGATCGAAACCAC-
                                                                                                                                                                                ------AAGGTCACCCTCCCACCTTCATGCGTAGTAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 136-150 AND 308-317
                                                                                                         151 ATGAAGCTAAACTATGAGGTCATGACTAAACTAGGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-13 AND 184-201, AND ACETYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 AA
US-09-975-856-1 (1-576) x REP1_MOUSE (1-743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 ------488 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 oLeuThrGlyProGlyPro 147
                                                           11 TyrPheGlyArgSerGlnPhe-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 185-207.
                                                                                                                                                                                                                                                                                                                                271 -----
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385 CCTCTGGCACTTCCTTCAAACCATTTTCTTCCTCTGCTGGCTTCTTGGGCAIGATCTTCG 326
                                                                                                                                                                              265 TTCGATCGTTACCAAAATCATTCCCGTGGAAGTCTGCAGCCCGTTTACTACGCATGAAAG 206
                                                                                                                                                                                                                                                                                                                                                  103 eGlnPheLysThriysValCysSerValThrLysHisGluAspPheAsnThrThrGlyGl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTISSUB-Brain, and Lymph;

WEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=1247, Mex., Scheefer C.F., Bate S.F., Garana C.F., Bate B., Garana C.F., Bate S., Carninol P., Mullahy S.J., Boraken P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley C.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., Worley C.M., Sodergren E.J., Lu X., Gibbs R.A., Millahon D.K., Muzmy D.M., Sodergren E.J., Lu X., Gibbs R.A., Willahon D.K., Muzmy D.M., Sodergren E.J., Lu X., Gibbs R.A., Millahon D.K., Marny D.M., Sodergren E.D., Dickson M.C., Antking M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Malkealey R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Medling D.E., Menerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Menterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Medling D.E., Menerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Menterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M., Menerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Menterfield Y.S.N., Marywinski M.I., Skalska U., Smailus D.E., M., Menerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Menterfield Y.S.N., Marywinski M.I., Marra M.A., Marra M.A., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Scheil J.E
                                                                                                                                         325 GGAAGATTCTCTGGAGGCTGCCGAAAGTCATCTGAGGACGTTCAACCTGATTCCTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096077; QBNDR7; QBWU62; Q9BXY9;
10-007-2003 (Rel. 42, Created)
10-007-2003 (Rel. 42, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
RalBP1 associated Eps domain containing protein 1 (RalBP1-interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bloecker H., Boecher M., Brandt P., Mewes H.-W., Weil B., Wiemann S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: May coordinate the cellular actions of activated EGF receptors and Ral-GTPases (By similarity).

-!- SUBUNIT: Homodimer (Potential). Interacts with RALBPI, CRK and GRB2. Binding to RALBPI does not affect its Ral-binding activity. Forms a complex with the SH3 domains of CRK and GRB2 which may link it to an EGF-responsive tyrosine kinase (By similarity).

-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MAGO Y., Xiet Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang Tang R., Chen X., Wu C.;
Submitted (MAR-2000) to the EWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         744 AA.
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123 nTrpAsp 125
                                                                                                                                                                                                                                                                                                                                                                                                                         205 GTGGGAG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          565 ACTCGTCATCTTCCTCAGGGTCGCTGATCTCTTCATAAACCACCAGCTGCTTTCTCTCAC 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οŧ
                                                                                                    of
                      MEDLINE=95278229; PubMed=7758472;
Wu R.-F., Ichikawa Y.;
Ma essential lysyl residue (Lys208) in the substrate-binding site porcine FAD-containing monoxygenase.";

Fur. J. Biochem. 229:749-753(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem. Res. Toxicol. 11:1145-1153(1998).
-!- FUNCTION: This protein is involved in the oxidative metabolism a variety of xemobiotics such as drugs and pesticides.
-!- CATALYTIC ACTIVITY: N,N-dimethylaniline + NADPH + O(2) = N,N-dimethylaniline N-oxide + NADP(+) + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HIGH MANNOSE).
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InterPro; IPR00159; PAD_pyr_redox.
InterPro; IPR001960; Plav_cont_mnoxgn.
Pfam; PF00743; FM0-11kev [1.]
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00340; FADPNR.
PRINTS; PR00370; FMOXXGENASE.
Oxidoreductase; Monooxygenase; NADP; Flavoprotein; FAD; Microsome; Transmembrane; Multigene family; Acetylation; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                 "N-glycosylation of pig flavin-containing monooxygenase form 1: determination of the site of protein modification by mass spectrometry."; Chem. Res. Toxicol. 11:1145-1153(1998).
                                                                                                                                                                                                                                                                        MEDLINE=98451545; PubMed=9778310;
Korsmeyer K.K., Guan S., Yang Z.C., Falick A.M., Ziegler D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||
|ThrGluHisValGluGluGlyArgAlaSerLeuTyrLysSerVal---
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Microsomal.
-!- TISSUE SPECIFICITY: Liver.
-!- SIMILARITY: Belongs to the FMO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLATION.
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195 NA
207 SU
119 NA
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PIR; A33768; A33768.
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531 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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CARBOHYD
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CCTGG 492

-----GluProAla 109

---AspThr 96

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    CAGATGACTTTCGGCAGCCTCCAGAGAATCTTCCCGAAG 330
                                                         391 GGCCCACAAAATGATGGGAAACAGCTGTGCCCCCGGGAAATCCAAGTACCTTGGAGAAG 450
                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              undifferentiated proliferating cells of neural epithelium. A greater expression is seen in the maturing neurons after they leave the neural epithelium. It is also found in the gut epithelium and adrenal medulla. SIMILARITY: Contains 1 HMG box domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Embryonic expression of the chicken Sox2, Sox3 and Sox11 genes suggests an interactive role in neuronal development.";
Mech. Dev. 49:22-36(1995).
-!- FUNCTION: 19.22-36(1995).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Low level expression is seen in
                     TISSUE=Embryo;
MEDLINE=59267693; PubMed=7748786;
Wanogho D., Rex M., Cartwright E.J., Pearl G., Healy C., Scotting P.J., Sharpe P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 ATTAACAAGACATCTGGACCCAAAAGGGGGAAACATG-----
                                                                                   97 ValGlnProArgThrSerAlaAspAlaGln-----
                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FRE-1996 (Rel. 31, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Transcription factor SOX-11.
                                                                                                                                                                                                                                                                                                             396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HMG BOX.
POLY-ALA.
POLY-GLU.
POLY-PRO.
POLY-ARG.
                                                                                                                                                                                                                                                                                                             PRT;
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PIR; 150707; 150707.
HSP: P40436; 1509.
InterPro; IPR000910; HMG_12_box.
                                                                                                                                                                                                                                                                                                             STANDARD;
    283 GAACGICCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                           493 ACCC 496
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                                                                                                                                                                                                                                                                                                             CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACTICICIAAGAAAGAGIGGGAAAAGAIGAAATCCICGGAGAAAATCGICIAIGIGIAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 CGGGCTGCAGACTTCCACGGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3).
3F. 2; AAH12764).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AAGGICACCCICCCACCITICAIGCGIAGIAAA-----
                                                                 PTM: EGF stimulates phosphorylation on Tyr-residues (By similarity).
                                                                                            -!- SIMILARITÝ: Contains 1 EH domain.
-!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COILED COIL (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_007954.
Missing (in 1seform 3).
/FTId=VSP_007955.
A -> V (IN REF. 1).
V -> I (IN REF. 3).
SH -> FP (IN REF. 2, AAH127).
W; 1DFF29711DB2B5E4 CRC64;
             Name=2;
IsoId=Q96D71-2; Sequence=VSP_007953, VSP_007954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH RALBPI
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Missing (in isoform 2).
'mmrd=VSP_007954.
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339
24
24
31
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EF-HAND (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                      IsoId=Q96D71-3; Sequence=VSP 007955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
 isoId=Q96D71-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-975-856-1 (1-576) x REP1_HUMAN (1-744)
                                                                                                                                                                                                                                               EMBL; AF251052; AAK34942.1; -.
EMBL; BC012764; AAH12764.1; -.
EMBL; BC021211; AAH21211.1; -.
EMBL; AG31900; CAD38569.1; -.
Genew; HGNC:15578; REPS1.
InterPro; IPR002048; EF-hand.
InterPro; IPR002061; EPS15_homology.
                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PS00018; BF HAND; 1.
PROSITE; PS50031; BH; 1.
Calcium-binding; Coiled coil;
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87.00
38.89%
24.07%
8.49%
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SMART; SM00027; EH: 1
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739
236
394
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Percent Similarity:
Best Local Similarity:
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600
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CONFLICT
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MEDLINE=22388257; PubMed=12477932;
      ---AAACGGGCTGCAGACTTCCACGGGAATGATTTTGGTAACGATCGAAACCACAGGAAT 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 CAGGITGAACGICCICAGAIGACIITICGGCAGCCICCAGAGAAICITCCCGAAGAICAIG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 CCCAAGAAGCCAGCAGAAGAAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 ProLysMetAspProSerAlaLysProAsnAlaGlyGlnSerProGluLysAsnAlaPro 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 CAAAAIGAIGGGAAACAGCIGIGCCCCCGGGAAAICCAAGIACCIIGGAGAAGAITAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                             115 AAGATGAAATCCTCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ProphelleArgGluAlaGluArgLeuArg 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ProArgLysLys 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 GlyGlyGlySerLysSerAlaLysSerSerGlyLysLysCysSerLysLeuLysAlaAla 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 AlaAlaSerProProLysProGlyAlaLysAlaAlaProHisGlyAspTyrAlaGlyAsp 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -AGACTGCGTGAGAGAAGCAGCTGGTGGTTTAT 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 GluTyrValPheGlyAlaLeuLysValSerSerLysAlaValLysCysValPheValAsp 203
                                                                                                                                                                                                                                                       25 AGGAGACCCAGGGATGATGCTCAAATATCAGAGAGTTA-----CGAAAGGCCTTCGAT 78
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LysArgProMetAsnAlaPheWetValTrpSerLyslleGluArgArgLyslleMetGlu 69
                                                                                                                                                                                                                                                                                                                                          GATATTGCCAAATACTTCTAAGAAAGAGTGGGAA
                                                                                                                                                                                                                                                                                                                                                                   175 ACTAAACTAGGTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGT--------
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZN38 HUMAN STANDARD; PRT; 446 AA.
P17036; P13683; Q9NXS; Q9NXJ; Q9UC15; Q9UC16;
O1-ARP-1990 (Rel. 14, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 38 (Zinc finger protein KOX25) (Zinc finger protein HF.12) (Zinc finger protein 3) (HZF3.1 protein).
Homo sapieng (Human).
  8E4B0A457F8BA833 CRC64;
                                                                 396
45
22
67
77
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                                                                                Matches:
Conservative:
Mismatches:
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                                                                                                                                                  Indels:
                                                                                                                                                                                                                 (1-396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetLeuLysAspSerGluLysile----
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43503 MW;
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TISSUE=Ovary, and Skin;
396 AA;
                                                                                                                         Best Local Similarity:
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                                                                                                       Percent Similarity:
                                          Alignment Scores:
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SEQUENCE
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                                                                                                                                               Query Match:
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ZN38 HUMAN
LD ZN38 HU
AC P17036 H
DT 20-PEB-
DT 20-PEB-
DT 20-PEB-
DE Zinc fi
DB Zinc fi
DB Zinc fi
CN ZNP38 C
CO ENKALY
CO ENKALY
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Altaushers R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., Stapleton M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J., Rownstein M.J., Usdin T.B., Potshyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McKernan R.J., Malek J.A., Gunaratne P.H., Allahan D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Butfard G.G., Bakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rohnert J., Myers R.M., Rahing W., Scherchield Y.S.N., Krzywinski, M.I., Skalska U., Smailus D.E., Schnertield Y.S.N., Krzywinski, M.I., Skalska U., Smailus D.E., Human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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-:- FUNCTION: INVOLVED IN CELL DIFFERENTIATION AND/OR PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pannuti A., Lanfrancone L., Pascucci A., Pelicci P.G., la Mantia G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thiesen H.-J.;
"Multiple genes encoding zinc finger domains are expressed in human
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosati M., Marino M., Franze A., Tramontano A., Grimaldi G., "Members of the zinc finger protein gene family sharing a conserved N-terminal module.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Colon mucosa;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., 180gai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 19:5661-5667(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC011887; AAH11887.1; ALT_INIT.
EMBL; BC013603; AAH13603.1; ALT_INIT.
EMBL; X60123; CAB4195.1; -
EMBL; AX000223; BAA91019.1; -
EMBL; X52356; CAA35582.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92051312; PubMed=1945843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88247738; PubMed=3380682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91145339; PubMed=2288909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
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196 ACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGGACTTCCACGGGAATGATTTTGGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 GTCTATGTGTATATGAAGCTA---AACTATGAGGTCATGACTAAACTAGGTTTCAAGGTC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AAICAGGIIGAACGICCICAGAIGACIIIC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ATCATGCCCAAGAAGCCA 348
                                                                                                                                                                                                                                                                                                                                                                                  79 GATATTGCCAAATACTTCTCTAAGAAAGAGTGGGAAAAGATGAAATCCTCGGAGAAAATC 138
                                                                                                                                                                                                                                                                                                                                                                   35 AspGluMetLeuAlaAlaAlaLeuLeuLysAlaLysSerGlnGluLeuValThrPheGlu 54
                                                                                                                                                                                                                                                                                                                                                                                          -----TTCGAT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GlyAshValPheSer 89
  L -> P (IN REF. 2).

GEKPY -> IRDSG (IN REF. 5).

GEKPYENCHEGGRAFESGENHYGHORIHTGEKPYECHGGK

FEYSSGLIGHQ -> EALPTFVTLIRLLESVDPIVTNEAAF

PASSLATIPALIWELFCVHSGLMFKKV (IN REF. 3).

67A6926807304782 CRC64;
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442
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Conservative:
Mismatches:
Indels:
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86.50
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EMBL; X07290; CAA30269.1;
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Best Local Similarity:
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Ωp	110	110 GlyValLeuLeuGlyArgPheGlnLysAspileSerGlnGlyLeuLysPheLysGluAla 129	53
à	349	349 GCAGAGGAAGAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGG 408	80
qq	130		138
à	409	AAACAGCTGTGCCCCCCGGGAAATCCAAGTACCTTGGAAAAATTAACAAGACATCTGGA 46	68
QQ	139		20
70	469	469 CCCAAAAGGGGGAAACATGCCTGGACCCAACAGACTGCGTGAGAGAAAGCAGCTGGTGGTT 528	28
Dp	151	.::::: :::	09
λö	529	TATGAAGAGATCAGCGACCCTGAGGAAGATGACGAG 564	
οp	161		

Search completed: March 31, 2004, 13:58:04 Job time : 18 secs

Perfect score:

Sequence:

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Run

Scoring table:

Minimum DB Maximum DB

sapien musculu musculu sapien

homo homo

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00024 mus musculu 08c523 mus musculu 08c523 mus musculu 075101 homo sapien 08i230 homo sapien 08i290 homo sapien 08i290 homo sapien 08i290 homo sapien 08i290 homo sapien 08c20 homo sapien 08c20 homo sapien 08c20 homo sapien 08c22 mus musculu 08uv31 homo sapien 09uld5 homo sapien 09uld5 homo sapien 09uld5 homo sapien 09uld5 homo sapien 09wvio mus musculu 08wvio mus musculu 08bvio mus musculu 08c64 mus musculu
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Q8tuh2 methanosarc
Q8tron methanosarc
Q8traO methanosarc
Q8tl12 methanosarc
Q8tl12 methanosarc
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
GO:0002818; AH02818.1.
GO:0005625; F:uncleic acid binding; IEA.
GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001569; KRAB.
InterPro; IPR003655; KRAB_related.
Ffam; PF01352; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                       096qil |
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09nzk4 |
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
Similar to synovial sarcoma, X breakpoint 2.
Homo sapiens (Human).
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TISSUE=Placenta;
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200.9
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   Q9BU88
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-Q=/cgn2_1/USPTO_spool_p/USO9975856/runat_31032004_132903_14748/app_query.fasta_1.775
-Q=/cgn2_1/USPTO_spool_p/USO9975856/runat_31032004_132903_14748/app_query.fasta_1.775
-Q=/cgn2_1/USPTO_spool_p/USO9975856/runat_31032004_132903_14748/app_query.fasta_1.775
-UNITS=bits -STRART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPNT=pc -NORM=sct -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=USO9975856 @CGN 1 1.86 @runat_31032004_132003_44748 -NCPU-6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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7733.553 Million cell updates/sec
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                                                                                                                                                                                                                          ATGAACGGAGACGACGTT.....ATGACGAGTAACTCCCCTCG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                 March 31, 2004, 13:40:37; Search time 47 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                  using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext (
Rgapop 6.0 , Fgapext (
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sp_bacteria:*
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sp_unclassified:*
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Match Length DB
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Database :

Score

No. Result

685.5

us-09-975-856-1.rspt

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155 AA
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                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                             Alignment Scores:
Pred. No.:
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                                                                                                                                                                        1 MetAsnGlyAspAspAlaPheAlaArgArgProThrValGlyAlaGlnIleProGluLys 20
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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2BF8E1FFA4D58094 CRC64;
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137
11
26
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Synovial sarcoma, X breakpoint 3.
                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                    US-09-975-856-1 (1-576) x Q9BU88 (1-223)
PS50806; KRAB RELATED;
           25173 MW;
                                              1.15e-62
685.50
66.07%
61.16%
66.88%
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           223 AA;
                                                                       Percent Similarity:
Best Local Similarity:
                                   Alignment Scores:
Pred. No.:
PROSITE;
SEQUENCE
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TISCHEB-Bone marrow;

A Strausberg R.; Translerg R.;

Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC005904; AAH05904.1; -.

EMBL; BC005004; AAH05904.1; -.

GO; GO:0000562; C:intracellular; IEA.

GO; GO:0000575; F:nucleic acid binding; IEA.

GO; GO:0000555; F:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR003655; KRAB.

R InterPro; IPR003655; KRAB.

R SMART; SM00349; KRAB; 1.

R SMART; SM00349; KRAB; 1.

R SMART; SM00349; KRAB; 1.

R SMART; SM00349; KRAB RELATED; 1.

R SGUENCE 170 AA; 19457 MW; D981F807A9C7EAB1 CRC64;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ54B20.1.1 (Novel SSX family protein (Isoform 1)) (Fragment).
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Matches:
Conservative:
Mismatches:
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us-09-975-856-1.rspt

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Alignment Scores:
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SerAspSerLysGlyValProGluAlaSerGlyProGlnAsnAspGlyLysLysLeuCys
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                                                                                                                DNA-dependent; IEA.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-DEC-2001 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ54B20.1.2 (Novel SSX family protein (Isoform 2)) (Fragment).
Grafham D.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; Z98304; CAC41946.1; ...
R GO; GO:0005622; C:intracellular; IEA.
R GO; GO:0003676; F:nucleic acid binding; IEA.
R GO; GO:0005355; P:regulation of transcription, DNA-dependen InterPro; IPR001909; KRAB.
R InterPro; IPR001909; KRAB.
R Ffam; PF01352; KRAB; I.
R SMART; SM00349; KRAB; 1.
R SMART; SM00349; KRAB; 1.
R Pfam; PF01155; KRAB; 1.
R SMART; SM00349; KRAB. 1.
R PAGSTIE; PS50806; KRAB. 1.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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Matches:
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005625; C:intracellular; IEA.
GO; GO:0005555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001909; KRAB.
InterPro; IPR003655; KRAB_related.
Pfam; PF01552; KRAB; I.
PROSTUR: DOCONONO.
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01-NOV-1999 (TERMELRE]. 12, Created)
01-NOV-1999 (TERMELRE]. 12, Last sequence update)
01-DEC-2001 (TERMELRE]. 19, Last annotation update)
SYT-SSX protein (Fragment).
SYT-SSX protein (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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545.50
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       US-09-975-856-1 (1-576) x QBWWZ9 (1-64)
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247.50
50.88$
45.61$
24.15$
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Clark J., Rocques P.J., Crew A.J., Gill S., Shipley J., Chan A.M.,
Gusterson B.A., Cooper C.S.;
"Identification of a novel genes, SYT and SSX, involved in the t(X;18)
(p11.2;q11.2) translocation found in human synovial sarcoma.";
NAt. Genet. 7:502-508(1994).
EMBL: X79200; CRB36970.1; -.
NON_TER
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
8A554H18.1 (Synovial sarcoma, X breakpoint 2) (Fragment).
SSX2.
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7014 MW;
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363.00
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NCBI_TaxID=9606;
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                                   [1]
SEQUENCE FROM N.A.
MEDLINE=20210694; PubMed=10749136;
dos Santos N.R., Torensma R., de Vries T.J., Schreurs M.W.J.,
dos Santos N.R., Torensma R., de Vries T.J., Schreurs G.W.J.,
de Bruijn D.R.H., Kater-Baats E., Ruiter D.J., Adema G.J.,
van Muijen G.N.P., Geurts van Kessel A.; rorensmans G.J.,
"Heterogeneous expression of the SSX cancer/testis antigens in human
melanoma lesions and cell lines.";
Cancer Res. 60:1654-1662(2000).
EMBL, AFI90791; AAF44724.1;
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41 IleHisGluArgSerGlyAsnArgGluAlaGlnGluLysGluGluArgArgGlyThrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 AA; 12399 MW; 981EBD852BA31DF8 CRC64;
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Matches:
Conservative:
Mismatches:
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86 ValTyrMetLysArgAsnTyrlleArgMetThrAspLeuGlyValThrValAsnGlnPro 105
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"Analysis of the mouse transcriptome based on functional annotation of
"C,770 [full-length CONSS.";
"Analysis of the mouse transcriptome based on functional annotation of
"C,770 [full-length CONSS.";
"A Nature 420:563-573 (2002).
"B EMBL; AK076879; BAC36519.1; -..
"B GO; GO:0005622; C:intracellular; IEA.
"GO; GO:0005625; P:racleic acid binding; IEA.
"GO; GO:00056355; P:regulation of transcription, DNA-dependent; IEA.
"R GO; GO:0005555; RRAB; I..
"R FRO3152; KRAB; I..
"R PRO3175; PS50805; KRAB; I..
"R PRO3175; PS508065; KRAB; I..
"R PRO5175; PS508065; KRAB; I..
------AspGluThrSerGlylleArg-----ValAsnValTrpSerHisArgLeu
                                                                                                           ArgGluArgLysTyrArgVallleTyrGluGluIleSerAspProGluGluGluGluArg
                                                                         CGTGAGAGAAAGCAGCTGGTGTTTATGAAGAATCAGCGACCCTGAGGAAGATGACGAG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical KRAB box/KRAB-related containing protein.
Mus musculus (Mouse).
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Matches:
Conservative:
Mismatches:
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TYBAIN-ECSTBL/60; TISSUE-Testis;
MEDIINE-22354683; PubMed=12466851;
The FANTOM COMBOTTIUM:
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214.50
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31.11%
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                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity:
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Pred. No.:
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Q8C5Z3;
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                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to Riken cDNA 4930414C09 gene.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Rodentia, Sciurognathi, Muridae, Musinae; MuscBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001909; KRAB.
InterPro; IPR001905; KRAB.
Ffam; PF01552; KRAB; 1.
PROSITE; PS508065; KRAB; 1.
PROSITE; PS508065; KRAB; 1.
PROSITE; PS50806; KRAB RELATED; 1.
SEQUENCE 128 AA; 15290 MW; F88614D1CBFF3B70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R., Strausberg R., Strausberg R., Strausberg R., Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BC0469421, AAH46441.1; CO, GO:0005622; C:intracellular, IEA. GO; GO:0005676; F:nucleic acid binding, IEA.
                       523
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                                       CATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGG
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214.50
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Best Local Similarity:
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DB:
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                                                                                                                                      24-26-021-11-0-02-02-11-0-02-02-11-0-02-02-11-0-02-11-0-02-11-0-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AsnLeuAlaGluThrGlyGlyIleGln--- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 GGGAAACATGCCTGGACCCACACAGACTGCGTGAGAAAGCAGCTGGTGGTTTATGAAGAG 537
                                                  --TTC 237
                                                                                                                                                                                                                                                                                                                                                        238 CACGGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 ACTITICGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAGGAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ValThrProlleLysArgMetLysLeu 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 GAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTG 417
                                                                            23 LysalaPheGlnAspIleSerThrTyrPheSerAspGluGluTrpGlyLysLeuThrGln 42
                                                                                                                                                                                                 43 TrpGlnLysSerAlaTyrValTyrMetLysArgAsnTyrIleArgMetThrAspLeuGly 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CAG
                                                                                                                                                                                                                                                                                                 ValThrValAsnGlnProValPheMetArgGlyLysGluGlnAlaLysGlnSerLeuVal
                                                                                                                                                                                                                                                                                                                                                                                        27 TCGGAGAAAATCGTCTATGTGTATATGAAGCTAAACTATGAGGTCATGACTAAACTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SSX-HSTT (Fragment).
SSX-HSTT.
SSX-HSTT.
Buno sapina (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCT
                                                                                                                                                                                                                                                      187 TTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGCTGCAGAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C9F9ADFCD0AD4542 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-975-856-1 (1-576) x Q9CPU1 (1-170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-975-856-1 (1-576) x 075101 (1-117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12611 MW;
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160.50
64.62%
52.31%
15.66%
                                                                                                                                                                                                                                                                                                                                                                                                     83 GludiyileGluVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerPheGly-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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"SSX-HSTT.";
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C STRAIN=C57BL/60; TISSUB=Testis;

MEDLINE=21085660; Dubmed=11217851;

A Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Saito T., Okazaki Y., Gojobori T., Bono H., Raukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Richi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

B Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

B Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

B Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Machima J., Mazzarelli J., Mombaerts P.,

A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Zato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynching-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                               :::::|||||||||||||||||-----AajaluThrSerflishrgLeu 142
                                                                                                                                                                                                                                                                                 GlyIle --- GluValHisAsp 126
                                                                                                                                                                                                                                                 CGTGAGAGAAAGCAGCTGGTGGTTTTATGAAGAGATCAGCGACCCTGAGGAAGATGACGAG 564
                                             385 GCATCTGGCCCACAAAATGATGGGAAACAGCTGTGCCCCCGGGGAAATCCAAGTACCTTG 444
                                                                                                                                                 445 GAGAAGATTAACAAGACATCTGGACCCAAAAAGGGGGAAACATGCCTGGACCCACAGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK015135; BAB29722.1; -.
BMBL; AK006218; BAB24465.1; -.
BMBL; AK006218; BAB24465.1; -.
MGI:1915235; 4930414C09Rik.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003576; F:mucleic acid binding; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001909; KRAB.
InterPro; IPR0030555; KRAB.related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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58
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Last annotation update)
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Indels:
Gaps:
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PS50806; KRAB RELATED;
170 AA; 19636 MW; F
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211.50
47.34%
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01-0TW-2001 (TrEMBLrel. 17,
01-0CT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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SMART: SM00349; KRAR.
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Pred. No.:
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DB:
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Alignment Scores:
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                                                                                                                                                                                                                            88 GluGlyAsnAspSerdluGluValProGluAlaSerGlyProGlnAsnAspGlyLysGlu 107
                                                                                                                                                                                        GAAGAAAATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAG 414
                                                            295 ATGACTITCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGCAGAAG 354
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53 GlyGlnGlnTyrGlyGlyTyrArgProThrGlnProGlyProProGlnFroProGlnGln 72
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Y.,
Nilsson G., Larsson O.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY138488; AAN39530.1; -.
NON TR 39 39
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Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Nilsson G., Larsson O.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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4336 MW;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                     8FC179F66C8C7E0D CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SS18/SSX2 fusion protein (Fragment).
SS18/SSX2 Fusion protein (Fragment).
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SS18/SSX2 fusion protein (Fragment).
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4336 MW;
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137.00
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75.76%
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EMBL, AY138489; AAN39531.1;

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SEQÜENCE 39 AA, 4336 MW;
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Search completed: March 31, 2004, 13:59:50 Job time : 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                    sw model
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March 31, 2004, 15:16:19 ; Search time 2745 Seconds
 (without alignments)
 6266.162 Million cell updates/sec Run on:

US-09-975-856-1

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Title:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

em estba:* EST: * Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			Match Length DB	1 1 1 1 1	979	836	887	863
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ALIGNMENTS

BM806411 979 bp mRNA linear EST 05-MAR-2002 AGENCOURT 6542819 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548810 5', mRNA Sequence.
BM806411.1 GI:19123234 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 979)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ArCc/DrD/DTP
Tissue Procurement: ArCc/DrD/DTP
Tissue Procurement. CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisoscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12258 row: f column: 11
High quality sequence stop: 622. Homo sapiens (human) ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 1 BM806411

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
(LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov.f column: 16
Plate: LLAM13525 row: f column: 16
High quality sequence stop: 624.
Location/Qualifiers
1. 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGACCAGCAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 TICGGCAGGCICCAGGGAAICTCCCCCGAAGAICAIGCCCAAGAAGCCAGGAGGAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 CCCCCGGGAAAICCAAGIACCTIGGAGAAGAITAACAAGACAICTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 CCCCCGGGAAAACCAACTACCTCTGAGAAGATTCACGAGAAGATCTGGACCCCAAAAGGGGG
  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 836;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                        /organism="Homo Bapiens"
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  AUTHORS
TITLE
JOURNAL
COMMENT
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AGENCOURT_7969283 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6165903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 836)
                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAACGGAGACGCCTTTGCAAGGAGACCCACGGTTGGTGTCTAATACCAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCCGGGAAAACCAACTACCTCTGAGAATTCACGAGAGATCTGGACCCAAAAGGGGG
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                                                                                                                                                                                                                                                                                                     DB 12;
                                                                                                                                                                                                                                                                                                     86.2%; Score 496.6; DB 12, 91.5%; Pred. No. 1.8e-131;
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                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                     organism="Homo sapiens"
                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5548810"
Location/Qualifiers
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AGENCOURT_1675894 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6035680 5', mRNA sequence.
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435 AATGATTCGGAGGAAGTGCCAGAAGCATCTGGCCCACAAAATGATGGAAAGAGCTGTGC 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="melanotic melanoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_72"
/note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Moverage insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 863)

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                                         CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGG
                                                                               cccceegaaaaccaacraccrcreagaagarrcaceagagarcregacccaaaaggese
                                                                                                                         481 AAACATGCCTGGACCCCACAGACTGCGTGAGAGAAGCAGCTGGTGGTTTTATGAAGAGATC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI3368 row h column: 17
High quality sequence stop: 625.
Location/Qualifiers
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91.2%; Pred. No. 7e-130;
iive 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6095680"
                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ222907.1 GI:20404307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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Matches 521; Conservative
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                                                987 bp mRNA linear BST 04-SEP-2002
.7858401 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6168477
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                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
Plate: LiAM13532 row: a column: 22
High quality sequence stop: 739.
                                                                                                                                                                                                                                                         1 (bases 1 to 887)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="melanotic melanoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:6168477"
                                                                                                                                  BU161779.1 GI:22675689
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Best Local Similarity 91.3%;
Matches 525; Conservative
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                                                                                 mRNA sequence.
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258 CTAGGITTCAAGGCCACCTCCCACCTTCATGTATAAACGGGCCGAAGACTTCCAG 317
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                                                                                       138 ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGTGGGAAAAGATG
                                                                                                                                                                                                            AAATCCTCGGAGAAAATCGTCTATGTGTGTATATGAAGCTAAACTATGAGGTCATGACTAAA
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             Pred, No. 3.7e
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                            521; Conservative
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/tissue_type="melanotic melanoma"
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/site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Revrage insert size 2 kb. Library constructed by Life
Technologies."
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1 (Dases 1 to 1001)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                               GCAGGCTCCAGGGAATCTCCCCGAAGATCATGCCCAAGAAGCCAGCAGAAGGAAAATG
                              GTTTCAAGGCCACCTCCCACCTTTCATGTGTAATAAACGGGCCGAAGACTTCCAGGGGA
                                                                    ATGATTTTGGTAACGATCGAAACCACGGAATCAGGTTGAACGTCCTCAGATGACTTTCG
                                                                                               241 ATGATTTGGATAATGACCCTAACCGTGGGAATCAGGTTGAACGTCCTCAGATGACTTTCG
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GTTTCAAGGTCACCCTCCCACCTTTCATGCGTAGTAAACGGGGCTGCAGACTTCCACGGGA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information of
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LIAM12233 row. i column: 22
High quality sequence start: 258
High quality sequence stop: 436.
Location/Qualifiers
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Tissue Procurement: ATCC/DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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bp mRNA linear EST 24-MAY-2002
Homo sapiens cDNA clone IMAGE:6159943
                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llh.gov row: n column: 08
High quality sequence stop: 634.
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AGGGACCCTGAGGAAGATGACGAGTAACTCCCCTC 652
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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AGENCOURT 7896851 NIH_MGC_72
5', mRNA Sequence.
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Length 1001;

DB 12;

84.8%; Score 488.6;

Query Match

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Laxon:9606"
/db_xref="Laxon:9606"
/dlone="INAGB:6051106"
/dlone="INAGB:6051106"
/lab_host=""Dh108 (phage-resistant)"
/dlone=1.b="NHH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 CTAGGTTTCAAAGTCACCCTCCCACCTTTCATGTGTAAAAACAGGCCACAGACTTCCAG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCCAGCAGCAGAAGAA 360
                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC/DCTD/DTP
Tissue Procurement: ATC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
Plate: LLAMM1304 row: g column: 11
High quality sequence stop: 696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAACGGAGGCCTTTGCAAGGAGACCCAGGGATGATGCTCAAATATCAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 ATGAACGGAGACGACCTTTGCAAAGAGACCCAGGGATGATGCTAAAGCATCAGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 83.6%; Score 481.6; DB 13;
Local Similarity 89.8%; Pred. No. 3.6e-127;
Les 517; Conservative 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655
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_7844770 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6051106
                                                                                                   /tissue_type="melanotic melanoma"
/lab host="PHIOB (phage-resistant)"
/clome lib="NHI MGC 72"
/note="Organ: skin, Vector: pCMV-SPORT6, Site_1: Not1;
/note="Organ: skin, Vector: pCMV-SPORT6, Site_1: Not1;
/note="Ingent skin, Vector: pCMV-sport6, Site_1: Not1;
/note: pCMM-sport6, Site_1: Not1;
/not
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Catarrhini; Hominidae; Howo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                              Score 481.6; DB 13;
Pred. No. 3.4e-127;
0; Mismatches 59;
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                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6159943"
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:22684226
                                                                                                                                                                                                                                                                                                                                                                           83.6%;
ilarity 89.8%;
Conservative
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5', mRNA sequence.
BU170242
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Matches 517; Conserv
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540 619 us-09-975-856-1.rst

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Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi; Eukaryota, Metazoa, Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Lases I to 1135)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1939)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: MGC Glone distribution information can be the distribution: MGC Clone distribution: MGC Clone distribution: MGC Clone distribution: MGC Clone distribution: Library Limiter Column: 07 http://image.llni.gov

Licality Sequence stop: 650.

Licality Sequence stop: 650.

Licality Qualifiers
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| / Organism="Homo sapiens" |
| mol_type="mRNA" |
| mol_type="mRNA" |
| db_xref="taxon:966" |
| / clone="IMAGB:3445470" |
| / doll_line="MGC36" |
| / dab_host="MGC36" |
| / lab_host="MHH MGC_10" |
| / clone="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                   BE535379 1135 bp mRNA linear BST 09-AUG-2000 601058532F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445470 5',
               CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAAGGGGGG 480
                                                                                                                         540
                                                                                                                                                        AAACATGCCTGGACCCACAGACTGCGTGAGAGAAAGAGCTGGTGGTTTTATGAAGAGATC 618
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                                                           CCCCCAGGAAAAGCAAATATTCTGAGAATTAATAAGAGATCTGGACCCAAAAGGGGG
                                                                                                              AAACATGCCTGGACCCCACAGACTGCGTGAGAGAAAGCAGCTGGTGGTTTATGAAGAGATC
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                                                                                                                                                                                                              AGCGACCCTGAGGAAGATGACGAGTAACTCCCCTCG 576
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E (bases I to 888)

I (bases I to 888)

I NIH-MGC http://mgc.nci.nih.gov/.

I National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be the principle of the Consortium/LINL at:

Floud through the I.M.A.G.E. Consortium/LINL at:

Flate: LLAM13530 row: j column: 22

High quality sequence stop: 636.

Location/Qualifiers
                         BQ432374 889 bp mRNA linear EST 24-MAY-2002
AGENCOURT 7859139 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6167925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="melanotic melanoma"
/lab_host="hH10B (phage-resistant)"
/clone_lib="NHH MGC_72"
/note="forgan: skin; vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 ATGAACGAGACGACCTTTGCAAAGACCCAGGGATGATGATGCTAAAGCATCAGAGAAG 138
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llarity 89.8%; Pred. No. 3.6e-127;
Conservative 0; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol_type="mRNA"
db_xref="taxon:9606"
                                                                                            BQ432374
BQ432374.1 GI:21171450
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/ Ab xref="taxon:9606"

/ Call line="Line="SNU-354+Cho-CK+Choi-CK+HLK-3"

/ Call line="SNU-354+Cho-CK+Choi-CK+HLK-3"

/ Lab host="Topl0F"

/ Lone="Organ: Liver; Vector: pT/T3-Pac; Site_1: EcoRI; Site_2: Not!; The library was contributed by the Soares laboratory and it was contructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research

6 (9): 791-8006. RNA was prepared from harvested cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim, M.R.,
                                                                                             360
                                                                                                                                                                                                                                                                                                                                                                                                                              CB158955 602 bp mRNA linear EST 30-JAN-2003
K-EST0218399 L18POOLIN1 Homo sapiens CDNA clone L18POOLIN1-32-F07
                             GGGAATGATTTTGGTAACGATCGAAACCACAGGAATCAGGTTGAACGTCCTCAGATGACT 300
                                                                                                                                                     420
                                                                                                                                                                                                      CCCCCGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCGAAAAGGGGGG 480
CTAGGTITCAAAGTCACCCTCCCACCTITCATGTGTAATAAACAGGCCACAGACTTCCAG 301
                                                                361
                                                                                                                  TTCGGCAGGCTCCACAGAATCATCCCGAAGATCATGCCCAAGAAGCCAGCAGGACGAA 421
                                                                                                                                                                   541
                                                                                                                                                                                                                                                                AAACATGCCTGGACCCACAGACTGCGTGAGAAAGCAGCTGGTGGTTTTATGAAGAGTC 540
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                     TTCGGCAGCCTCCAGAGAATCTTCCCGAAGATCATGCCCAAGAAGCCAGGAGAGAAGAA
                                                                                                                                                                                                                                482 CCCCCAGGAAAAGCAAATATTTCTGAGAAGATTAATAAGAGATCTGGACCCAAAAGGGG
                                                        302 GGGAATGATTTTGATAATGACCATAACGCAGGATTCAGGTTGAACATGCTCAGATGACT
                                                                                                                                              AATGGTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAAACAGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 602)

(Kim, N. S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 471.6; DB 14; Length 602; Pred. No. 2.2e-124;
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Vuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Bmail: yongsung@mail.kribb.re.kr
Blate: 32 row: F column: 07
High quality sequence stop: 602.
                                                                                                                                                                                                                                                                                                                           AGCGACCCTGAGGAAGATGACGAGTAACTCCC 572
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Unpublished (2002)
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CB158955.1 GI:28145081
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_7550845 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6066127
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ArCCDCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Library Arrayed by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lln/gov
Plate: LLAM13343 row: i column: 08
High quality sequence stop: 532.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 950)
                                                                                                                                                                                                                             ATCCAAAAGGCCTTCGATGATATTGCCAAATACTTCTCTAAGGAAGAGAGGAGAAAAGATG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                    Shiraki
                                                                                                                                                                                                                                                                                                                                                                                                         /close="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHl, Site_2: Sall-Xhol (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROY 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this
                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shirah
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://mage.lih.gov
Plate: LLAM.1751 row: e column: 09
High quality sequence stop: 790.
Location/Qualifiers
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90.1%; Pred. No. 2e-119;
-ivo n: Mismatches 54;
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                                                                                                                                                                                                                                                                                                              sapiens"
                       Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5296880"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="melanotic melanoma"
/lab host="HHUB (phage-resistant)"
/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dr
Average insert size 2 kb. Library constructed by Life
Technologies."
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I (bases 1 to 793)
NH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                          1 ATGAACGGAGACGCCTTTGCAAGGAGCCCAGGGATGATGCTCAAATATCAGAAAG
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603254435F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:5296880
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                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                                                            Score 470.8; DB 13;
Pred. No. 4.8e-124;
0; Mismatches 57;
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Matches 516; C
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BE408883 573 bp mRNA linear EST 21-JUL-2000 601303758F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637982 5',
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Contact: Robert Strausberg, Ph.D.
Email: capabs remail.nih.gov
Tissue Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov
Plate: LLCM338 row: d column: 15
High quality sequence stop: 571.
Location/Qualifiers
I. 573
//organism="Momo sapiens"
// mol type="mRNA"
// db xref="taxon:9606"
// clone="INAGE:8637982"
// issue Type="choricoarcinoma"
// issue Type="choricoarcinoma"
// issue Type="choricoarcinoma"
                                                                                                                                                                                                                                                     523
                                                                                                                                                                                                                                                                                                                                                             524 GAAACAIGCCIGGACCCACAGACIGGCGGAAAAAAAAAGCAGCIGGGGGATIITAIGAAGAGA 583
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 573)

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                                                                                                           404 AATGATICGAAGGGAGTGTCAGAAGCATCTGGCCCACAAAACGATGGGAAACAACTGCAC
                                                                                                                                                                                                                                                                                              480 GAAACAIGCCIGGACCCACAGACTGCGTGAGAGAAAGCAGCTGGTGG-TTTAIGAAGAGA
                                                                  AATGGTTTTGAAGGAAGTGCCAGAGGCATCTGGCCCACAAAATGATGGGAAACAGCTGTGC
                                                                                                                                                                                   CCCCCGGGGAAATCCAAGTACCTTGGAGAAGATTAACAAGACATCTGGACCCAAAA-GGGG
                                                                                                                                                                                                                                        464 CCCCCAGGAAAAGCAAATAATTCTGAGAAGATTAATAAGAGATCTGGACCCAAAAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases i to 5/2),
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.2e-110;
0; Mismatches 57;
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922 bp mRNA linear EST 02-MAY-2002
AGENCOURT_7560406 NIH_MGC_72 Homo Bapiens cDNA clone IMAGE:6048424
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NIH-MGC http://mgc.nci.nih.gov/.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC_72"
/note="Organ: skin, Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, Primer: Oligo dI
Average insert size 2 kb. Library constructed by Life
Technologies.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (CLONE)
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/Link at:
Plate: LiAM1327 row: g column: 17
High quality sequence stop: 483.
Location/Qualifiers
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Pred. No. 3.3e-117;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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867 bp mRNA linear EST 20-OCT-2000
6014334893F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919991 5',
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/mol_type="mixtor" baptens

/db_xref="taxon:9606"

/clone="lmAGE:3919991"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone lib="NIH MGC 72"

/clone lib="NIH MGC 72"

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/clone lib="NIH MGC 72"

/clone lib="xitor" bcMV-SPORT6; Site_1: Not1;

Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life

Technologies."
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1 (bases 1 to 867)
11H-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                             AAATCCTCGGAGAAAATCGTCTATGTGTATAAAGCTAAACTATGAGGTCATGACTAAA
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/organism="Homo sapiens"
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                                   Gaps
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         Length 867;
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        DB 10;
     Score 423.4; DB 10;
Pred. No. 1.9e-110;
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e : 2750 secs
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Query Match
Best Local Similarity 89.4
Matches 512; Conservative
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